FIG. 1

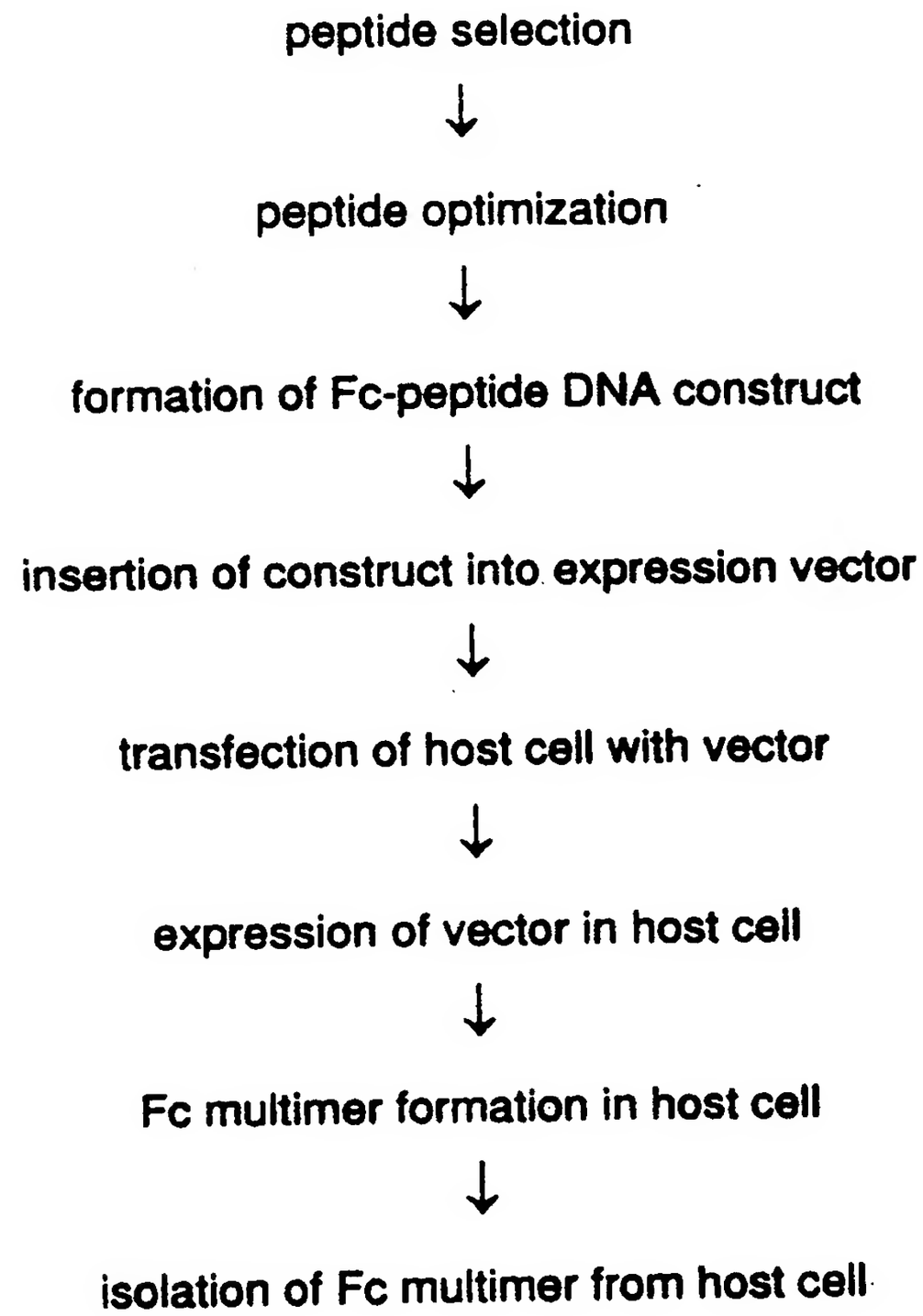
peptide selection
peptide optimization
formation of Fc-peptide DNA construct
insertion of construct into expression vector
transfection of host cell with vector
expression of vector in host cell
Fc multimer formation in host cell
isolation of Fc multimer from host cell

FIG. 2A

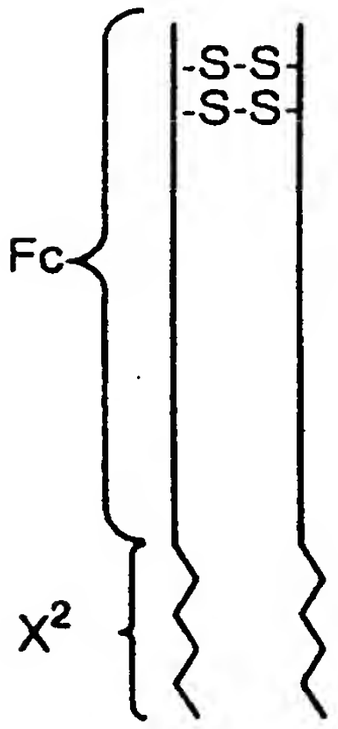

FIG. 2B

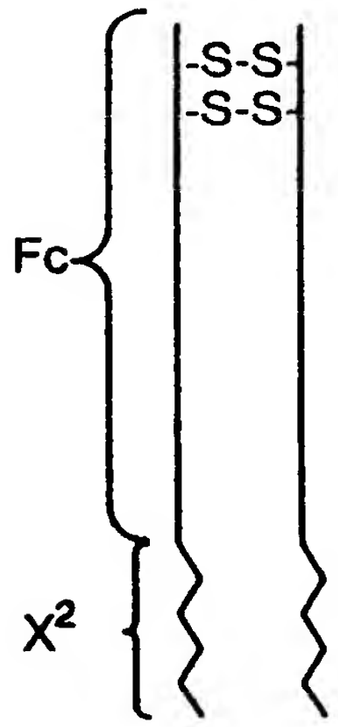

FIG. 2C

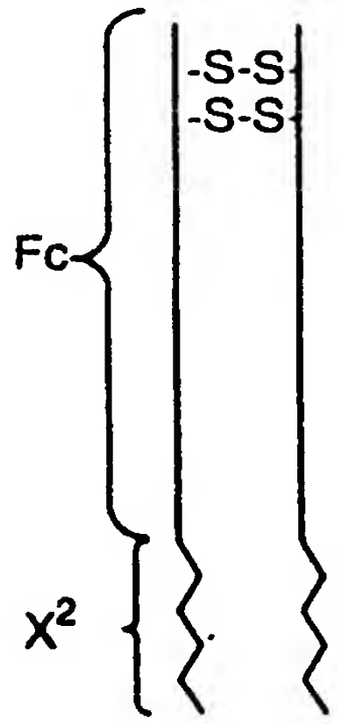

FIG. 2D

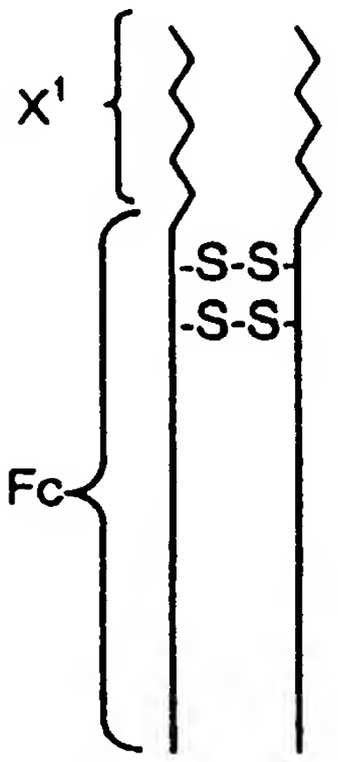

FIG. 2E

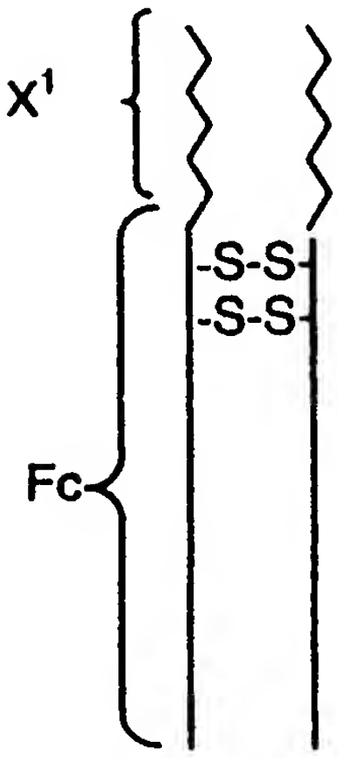

FIG. 2F

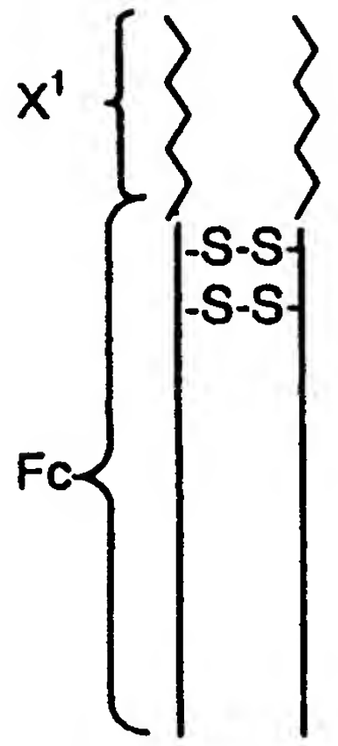

FIG. 3A

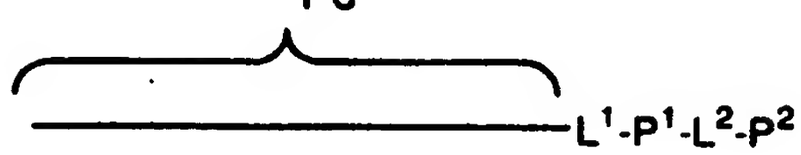

FIG. 3B

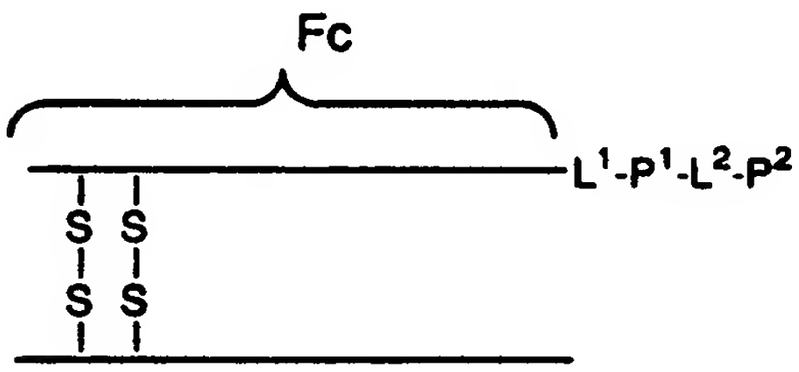

FIG. 3C

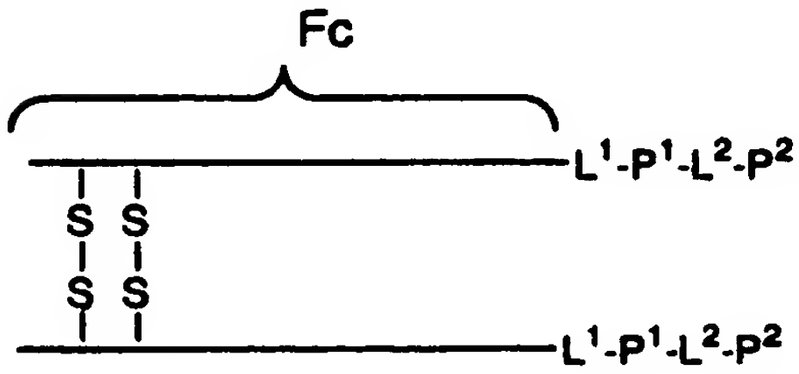

FIG. 4

```
                ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA
              1 ---------+---------+---------+---------+---------+---------+--------- 60
                TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a                 M   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   P   S   -

                GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
             61 ---------+---------+---------+---------+---------+---------+--------- 120
                CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a                 V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   V   -

                ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
            121 ---------+---------+---------+---------+---------+---------+--------- 180
                TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a                 T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   V   -

                GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
            181 ---------+---------+---------+---------+---------+---------+--------- 240
                CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a                 D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   T   -

                TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
            241 ---------+---------+---------+---------+---------+---------+--------- 300
                ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG

a                 Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   -

                AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
            301 ---------+---------+---------+---------+---------+---------+--------- 360
                TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a                 K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   -

                AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
            361 ---------+---------+---------+---------+---------+---------+--------- 420
                TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a                 K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   T   -

                AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
            421 ---------+---------+---------+---------+---------+---------+--------- 480
                TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a                 K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   V   -

                GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
            481 ---------+---------+---------+---------+---------+---------+--------- 540
                CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG

a                 E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   D   -

                TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
            541 ---------+---------+---------+---------+---------+---------+--------- 600
                AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a                 S   D   G   S   F   F   L   Y   S   K   L   T   V   D   K   S   R   W   Q   Q   -

                GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
            601 ---------+---------+---------+---------+---------+---------+--------- 660
                CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

a                 G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   K   -

                AGCCTCTCCCTGTCTCCGGGTAAA
            661 ---------+---------+----  684
                TCGGAGAGGGACAGAGGCCCATTT
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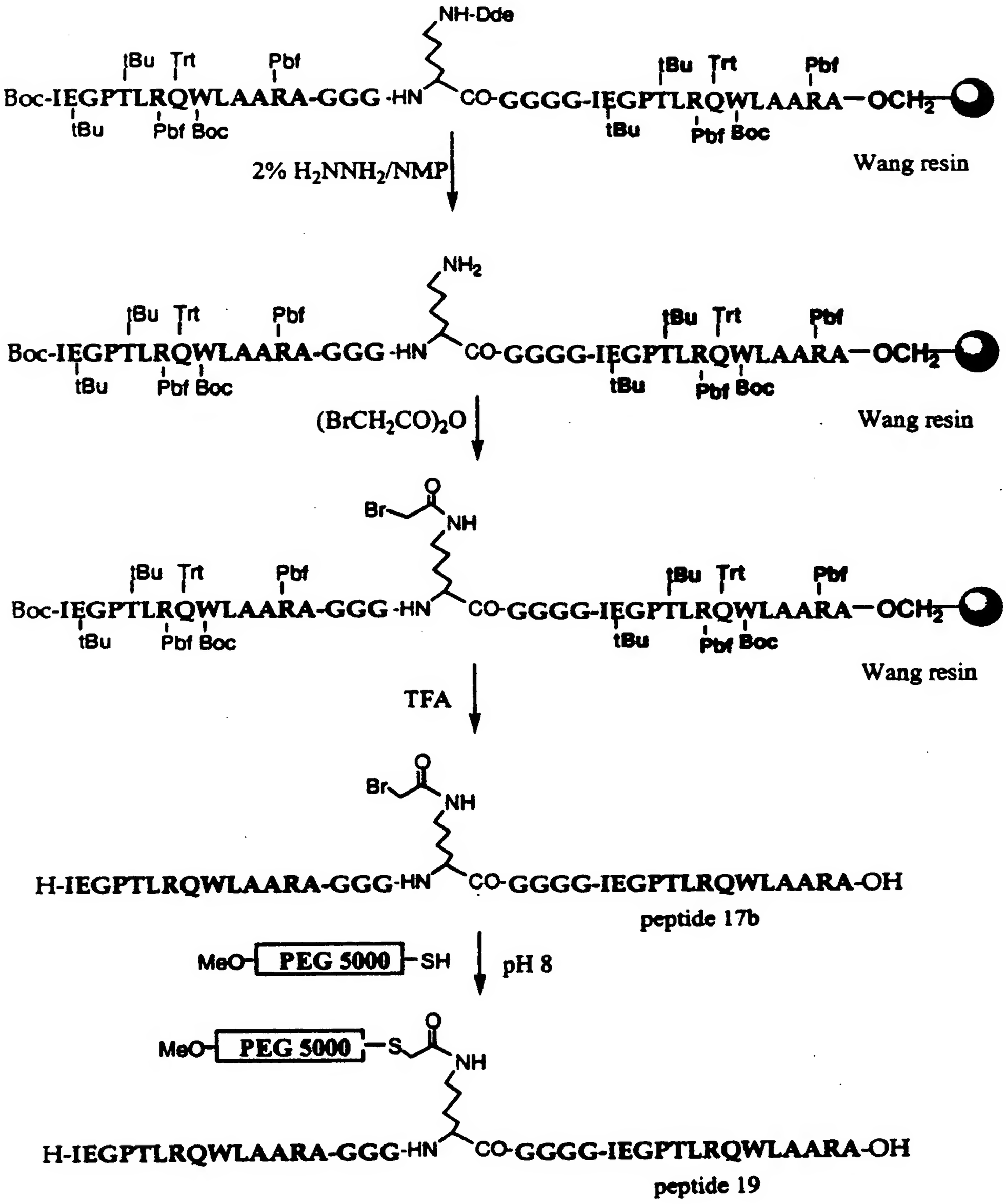
FIG. 5


NH-Dde
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Boc-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA—OCH2
tBu Pbf Boc
tBu Trt Pbf
tBu Pbf Boc
Wang resin
2% H2NNH2/NMP
NH2
(BrCH2CO)2O
Br
O
NH
TFA
H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH
peptide 17b
MeO PEG 5000 SH
pH 8
MeO PEG 5000 S
peptide 19

FIG. 6

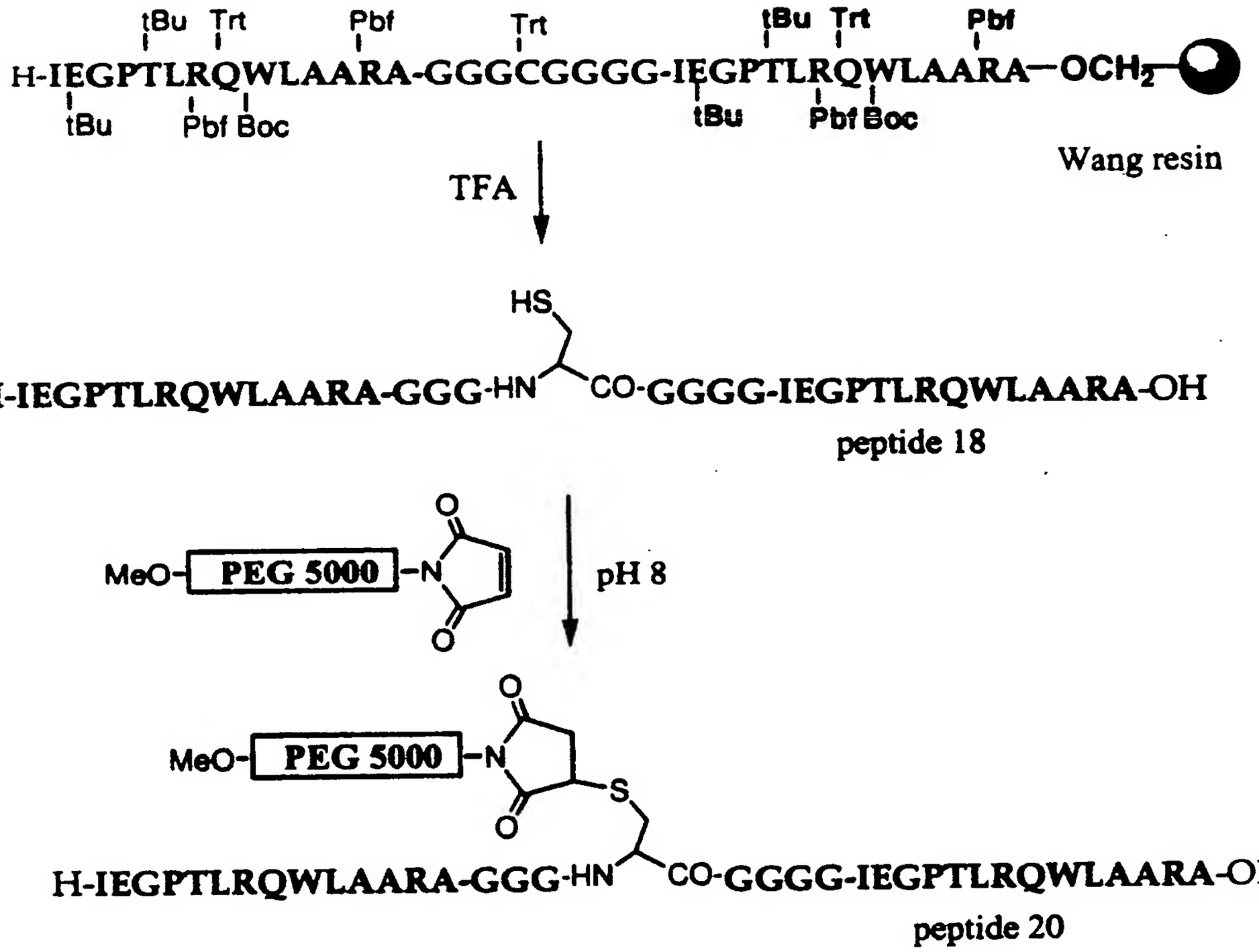
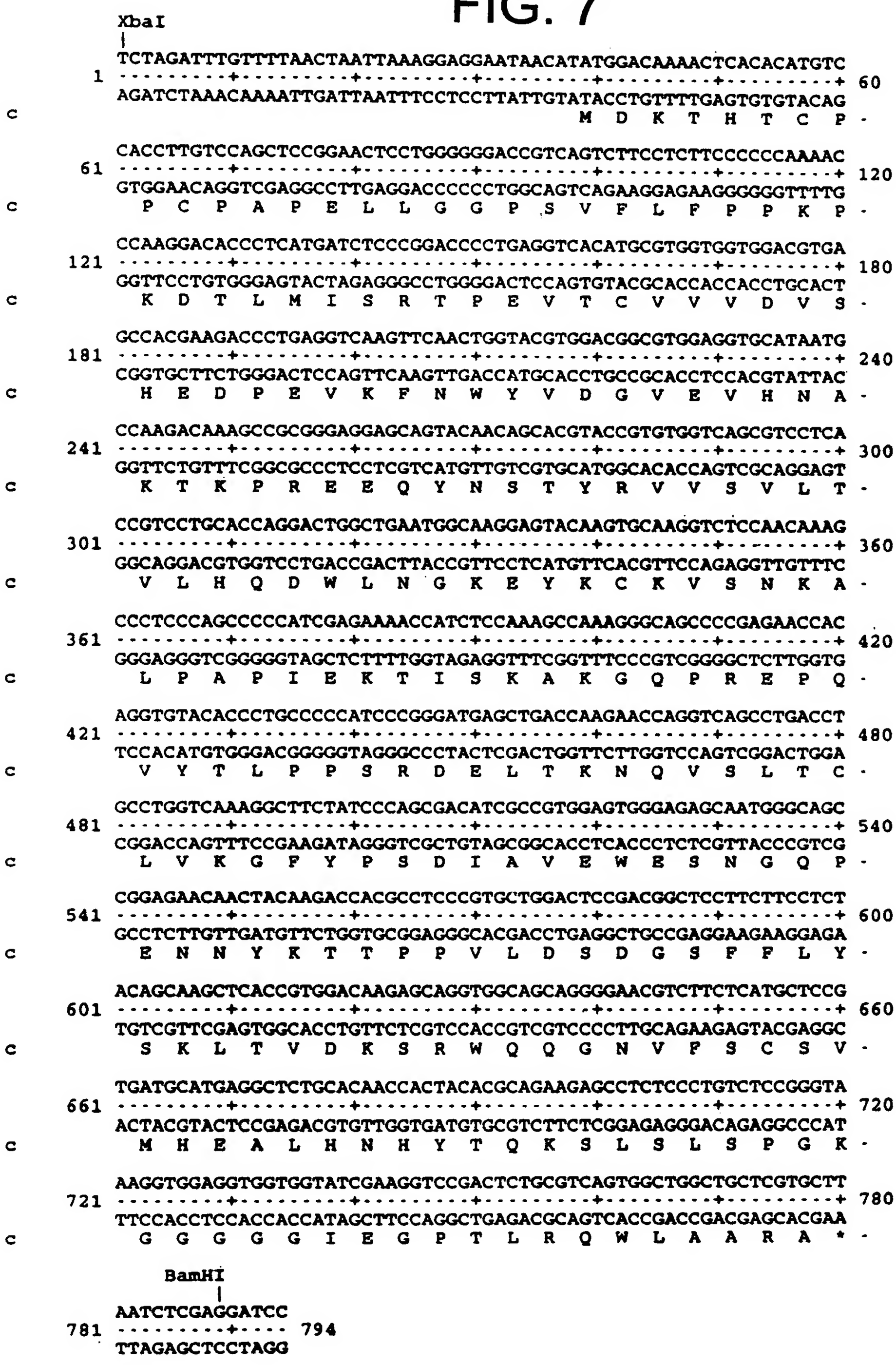

tBu Trt Pbf Trt tBu Trt Pbf
H-IEGPTLRQWLAARA-GGGCGGGG-IEGPTLRQWLAARA—OCH2
tBu Pbf Boc tBu Pbf Boc
Wang resin
TFA
HS
H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH
peptide 18
MeO- PEG 5000 -N
pH 8
MeO- PEG 5000 -N S
H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH
peptide 20

FIG. 7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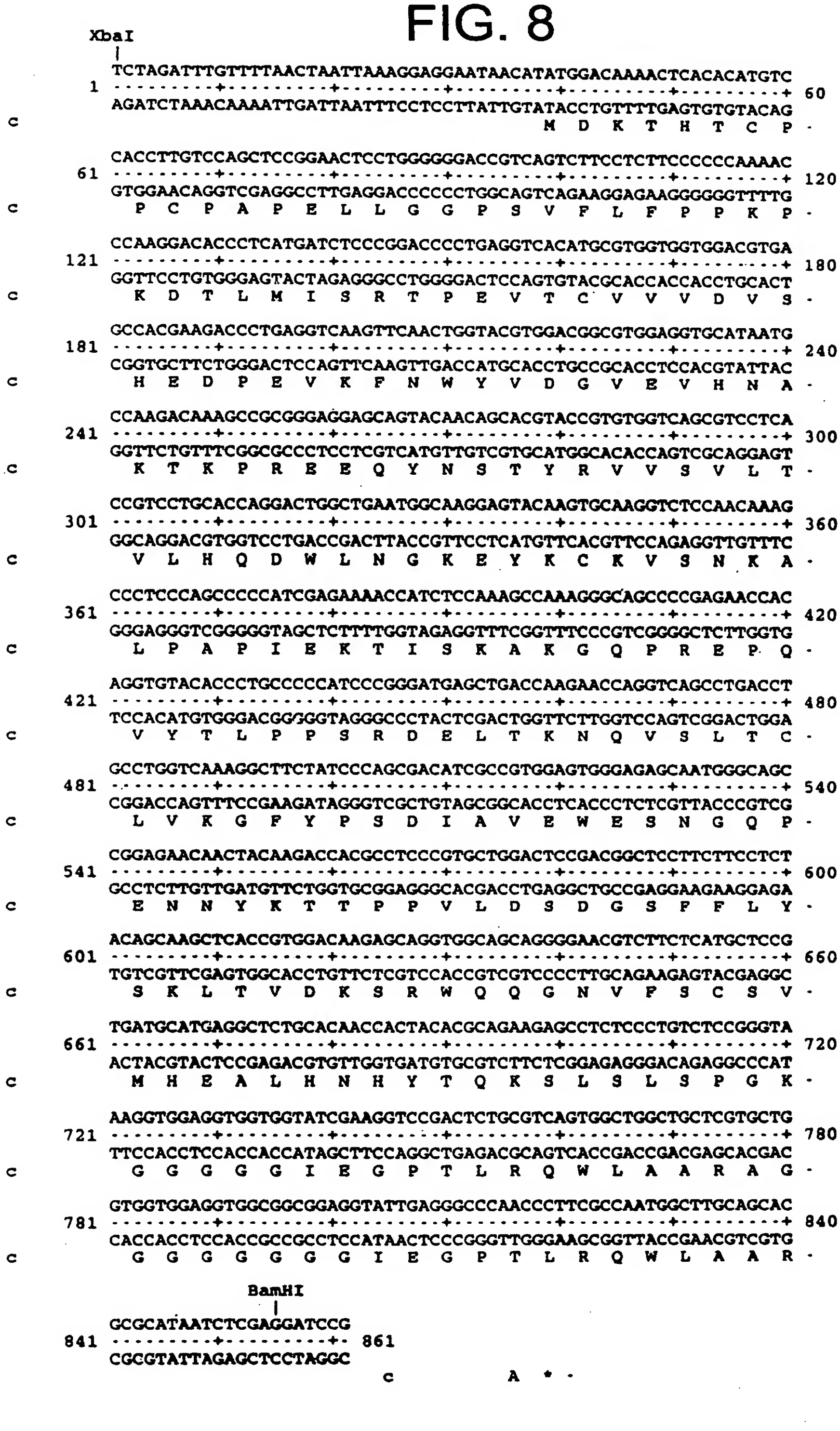
AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
c M D K T H T C P -
CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
c P C P A P E L L G G P S V F L F P P K P -
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
c K D T L M I S R T P E V T C V V V D V S -
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
c H E D P E V K F N W Y V D G V E V H N A -
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
c K T K P R E E Q Y N S T Y R V V S V L T -
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
c V L H Q D W L N G K E Y K C K V S N K A -
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
c L P A P I E K T I S K A K G Q P R E P Q -
AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
c V Y T L P P S R D E L T K N Q V S L T C -
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
c L V K G F Y P S D I A V E W E S N G Q P -
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
c E N N Y K T T P P V L D S D G S F F L Y -
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
c S K L T V D K S R W Q Q G N V F S C S V -
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
c M H E A L H N H Y T Q K S L S L S P G K -
AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTT
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAA
c G G G G G I E G P T L R Q W L A A R A * -
BamHI
AATCTCGAGGATCC
TTAGAGCTCCTAGG

FIG. 8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M D K T H T C P
CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q
AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K
AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTG
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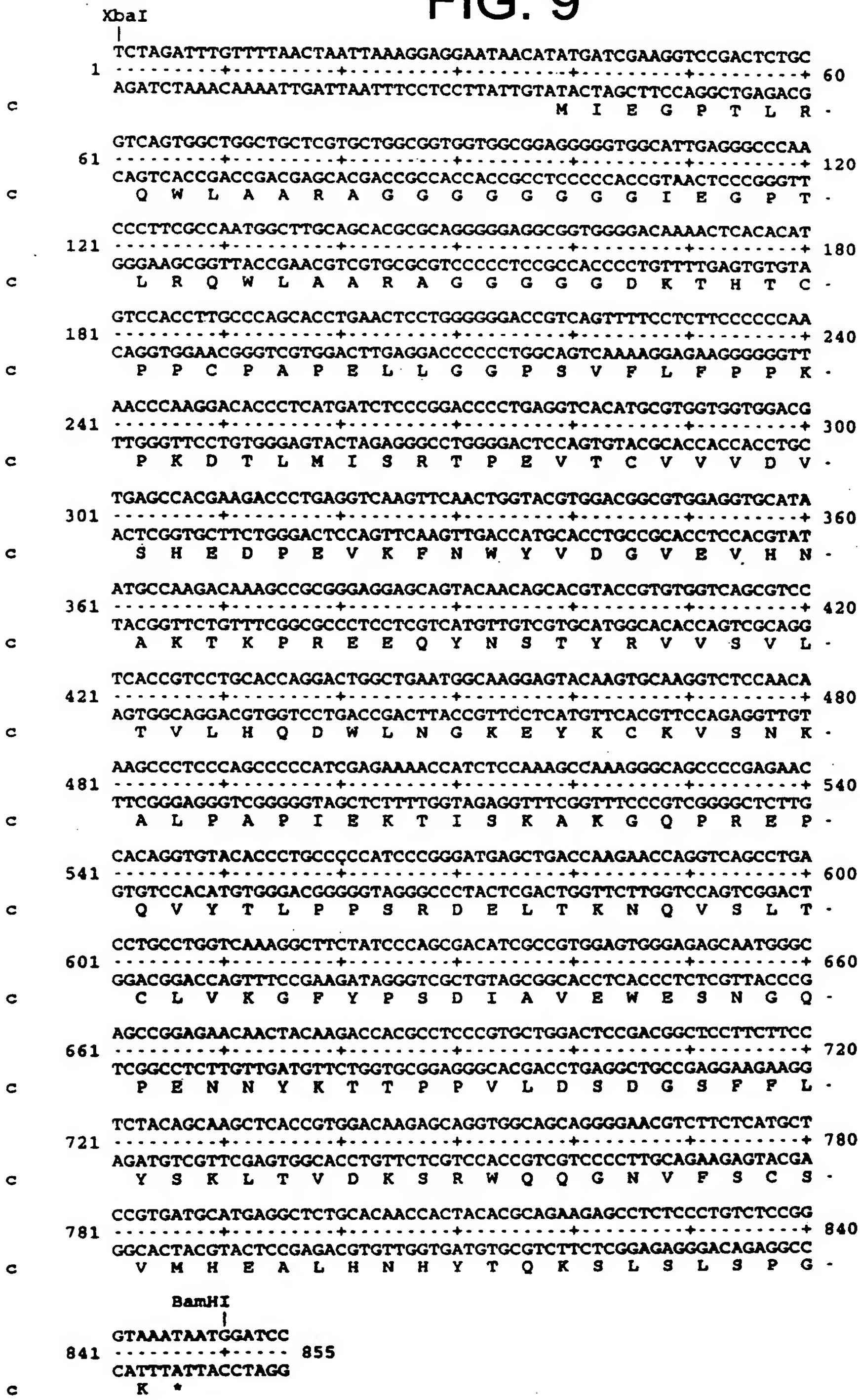
G G G G G I E G P T L R Q W L A A R A G
GTGGTGGAGGTGGCGGCGGAGGTATTGAGGGCCCAACCCTTCGCCAATGGCTTGCAGCAC
CACCACCTCCACCGCCGCCTCCATAACTCCCGGGTTGGGAAGCGGTTACCGAACGTCGTG
G G G G G G G I E G P T L R Q W L A A R
BamHI
GCGCATAATCTCGAGGATCCG
CGCGTATTAGAGCTCCTAGGC
C A * -

FIG. 9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AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R
GTCAGTGGCTGGCTGCTCGTGCTGGCGGTGGTGGCGGAGGGGGTGGCATTGAGGGCCCAA
CAGTCACCGACCGACGAGCACGACCGCCACCACCGCCTCCCCCACCGTAACTCCCGGGTT
Q W L A A R A G G G G G G G G I E G P T
CCCTTCGCCAATGGCTTGCAGCACGCGCAGGGGGAGGCGGTGGGGACAAAACTCACACAT
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L R Q W L A A R A G G G G G D K T H T C
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P P C P A P E L L G G P S V F L F P P K
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TTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGC
P K D T L M I S R T P E V T C V V V D V
TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
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S H E D P E V K F N W Y V D G V E V H N
ATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
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A K T K P R E E Q Y N S T Y R V V S V L
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
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T V L H Q D W L N G K E Y K C K V S N K
AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
TTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTG
A L P A P I E K T I S K A K G Q P R E P
CACAGGTGTACACCCTGCCCCCATCCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGA
GTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACT
Q V Y T L P P S R D E L T K N Q V S L T
CCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
GGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCG
C L V K G F Y P S D I A V E W E S N G Q
AGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC
TCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGG
P E N N Y K T T P P V L D S D G S F F L
TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT
AGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGA
Y S K L T V D K S R W Q Q G N V F S C S
CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCC
V M H E A L H N H Y T Q K S L S L S P G
BamHI
GTAAATAATGGATCC
CATTTATTACCTAGG
K *

FIG. 10

```
                XbaI
                 |
                TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
              1 ---------+---------+---------+---------+---------+---------+---------+ 60
                AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
c                                                       M   I   E   G   P   T   L   R -

                GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCGGTGGGGACAAAACTCACACATGTCCAC
             61 ---------+---------+---------+---------+---------+---------+---------+ 120
                CAGTCACCGACCGACGAGCACGACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
c                 Q   W   L   A   A   R   A   G   G   G   G   G   D   K   T   H   T   C   P   P -

                CTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCA
            121 ---------+---------+---------+---------+---------+---------+---------+ 180
                GAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGT
c                 C   P   A   P   E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K -

                AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC
            181 ---------+---------+---------+---------+---------+---------+---------+ 240
                TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG
c                 D   T   L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H -

                ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
            241 ---------+---------+---------+---------+---------+---------+---------+ 300
                TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT
c                 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N   A   K -

                AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCG
            301 ---------+---------+---------+---------+---------+---------+---------+ 360
                TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC
c                 T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S   V   L   T   V -

                TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
            361 ---------+---------+---------+---------+---------+---------+---------+ 420
                AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG
c                 L   H   Q   D   W   L   N   G   K   E   Y   K   C   K   V   S   N   K   A   L -

                TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
            421 ---------+---------+---------+---------+---------+---------+---------+ 480
                AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC
c                 P   A   P   I   E   K   T   I   S   K   A   K   G   Q   P   R   E   P   Q   V -

                TGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC
            481 ---------+---------+---------+---------+---------+---------+---------+ 540
                ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG
c                 Y   T   L   P   P   S   R   D   E   L   T   K   N   Q   V   S   L   T   C   L -

                TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
            541 ---------+---------+---------+---------+---------+---------+---------+ 600
                ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCC
c                 V   K   G   F   Y   P   S   D   I   A   V   E   W   E   S   N   G   Q   P   E -

                AGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACA
            601 ---------+---------+---------+---------+---------+---------+---------+ 660
                TCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGT
c                 N   N   Y   K   T   T   P   P   V   L   D   S   D   G   S   F   F   L   Y   S -

                GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
            661 ---------+---------+---------+---------+---------+---------+---------+ 720
                CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACT
c                 K   L   T   V   D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M -

                TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT
            721 ---------+---------+---------+---------+---------+---------+---------+ 780
                ACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA
c                 H   E   A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   G   K   * -

                 BamHI
                  |
                AATGGATCC
            781 --------- 789
                TTACCTAGG
```

FIG.11

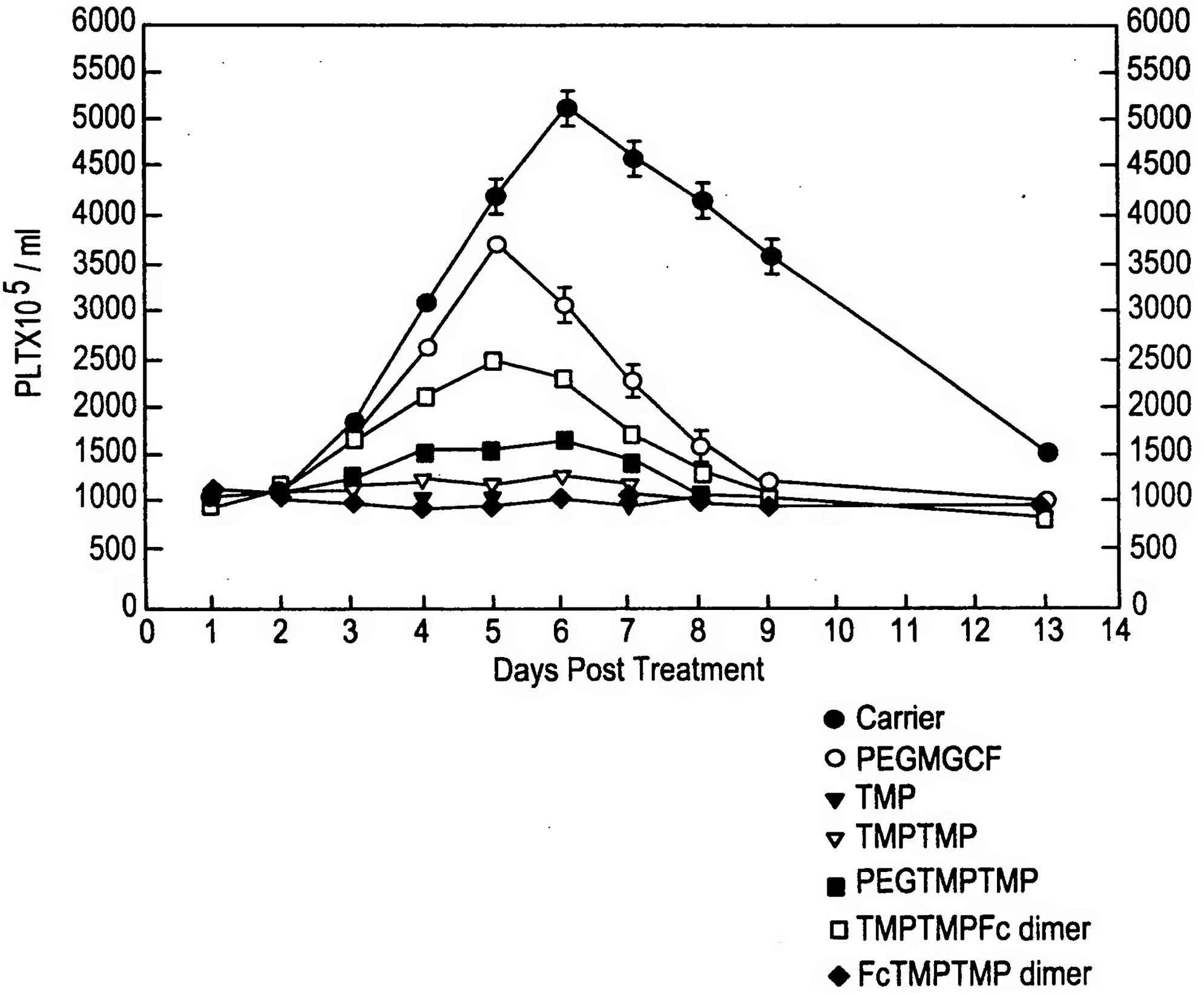

PLTX10^5/ml
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days Post Treatment
Carrier
PEGMGCF
TMP
TMPTMP
PEGTMPTMP
TMPTMPFc dimer
FcTMPTMP dimer

FIG.12

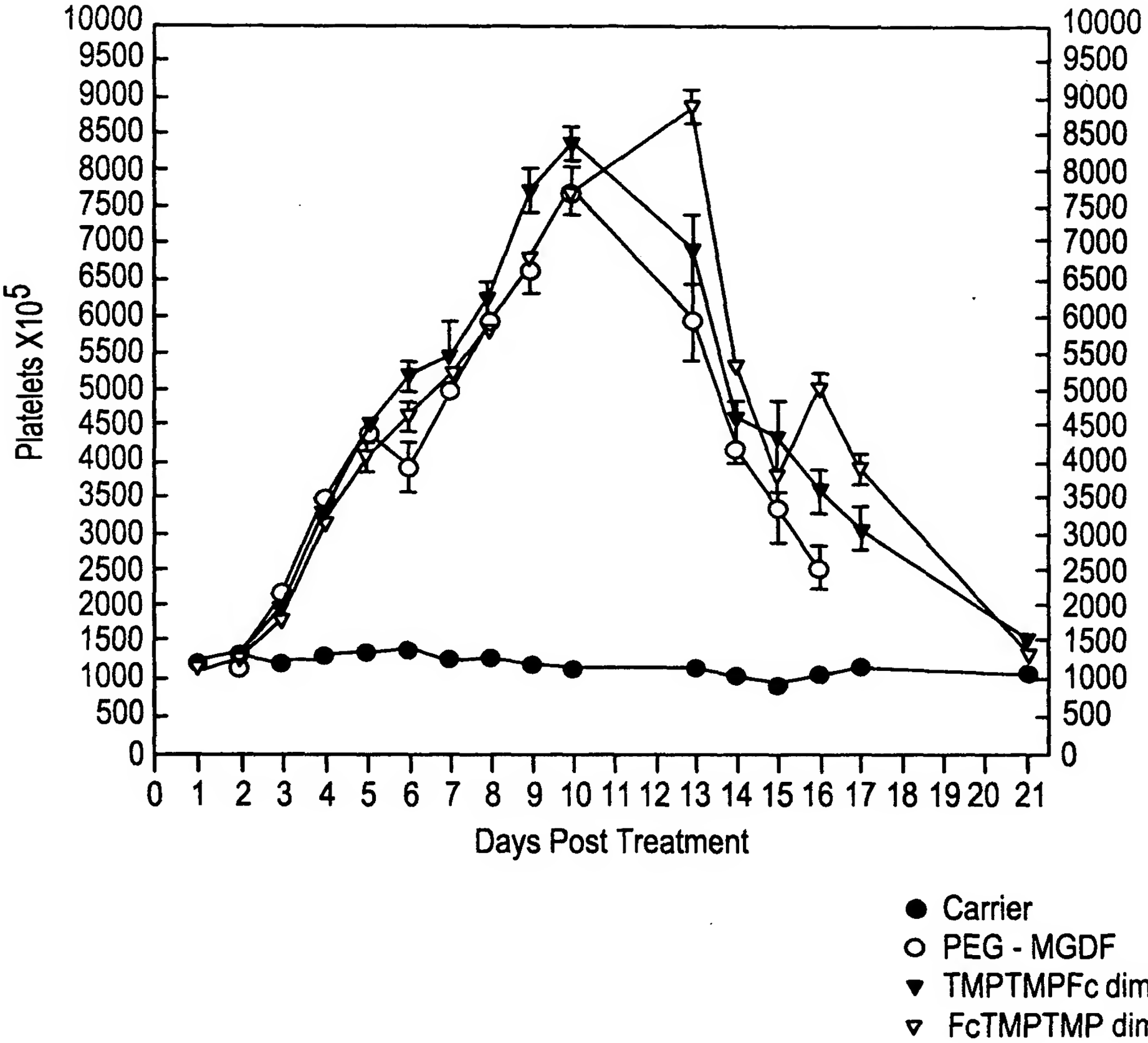

Platelets X10^5
10000
9500
9000
8500
8000
7500
7000
6500
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
Days Post Treatment
Carrier
PEG - MGDF
TMPTMPFc dimer
FcTMPTMP dimer

FIG. 13

```
                XbaI
                 |
                TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC
              1 ---------+---------+---------+---------+---------+---------+ 60
                AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
c                                                     M  D  K  T  H  T  C  P  -
                CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
             61 ---------+---------+---------+---------+---------+---------+ 120
                GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
c                  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  -

                CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
            121 ---------+---------+---------+---------+---------+---------+ 180
                GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
c                  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  -

                GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
            181 ---------+---------+---------+---------+---------+---------+ 240
                CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
c                  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  -

                CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
            241 ---------+---------+---------+---------+---------+---------+ 300
                GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
c                  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  -

                CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
            301 ---------+---------+---------+---------+---------+---------+ 360
                GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
c                  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  -

              CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
            361 ---------+---------+---------+---------+---------+---------+ 420
                GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
c                  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  -

                AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
            421 ---------+---------+---------+---------+---------+---------+ 480
                TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
c                  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  -

                GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
            481 ---------+---------+---------+---------+---------+---------+ 540
                CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
c                  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  -
                CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
            541 ---------+---------+---------+---------+---------+---------+ 600
                GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
c                  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  -

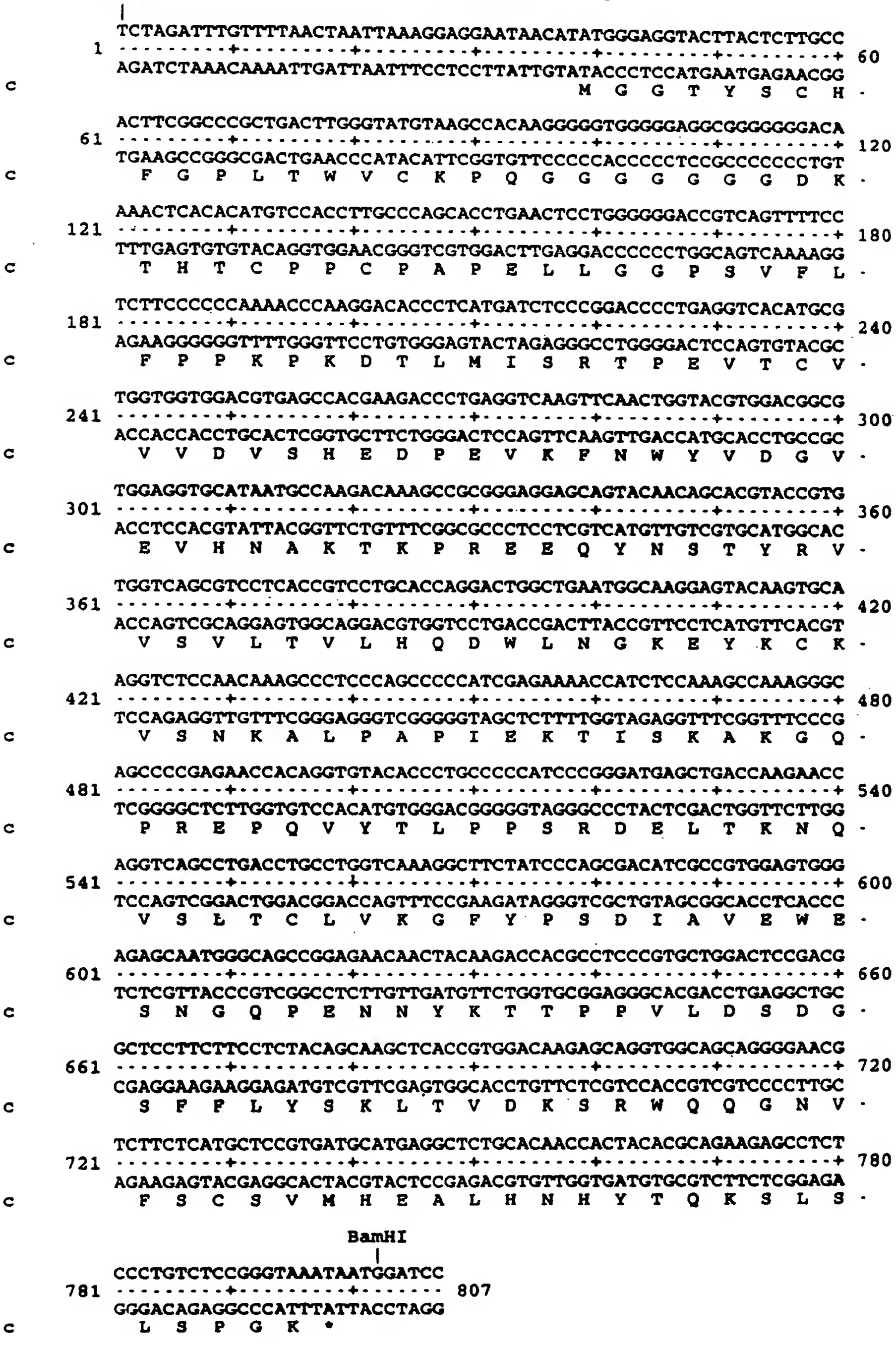
                ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
            601 ---------+---------+---------+---------+---------+---------+ 660
                TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
c                  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  -

                TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
            661 ---------+---------+---------+---------+---------+---------+ 720
                ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
c                  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  -

                AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT
            721 ---------+---------+---------+---------+---------+---------+ 780
                TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA
c                  G  G  G  G  G  G  G  T  Y  S  C  H  F  G  P  L  T  W  V  C  -

                                                BamHI
                                                 |
                GCAAACCGCAGGGTGGTTAATCTCGTGGATCC
            781 ---------+---------+---------+-- 812
                CGTTTGGCGTCCCACCAATTAGAGCACCTAGG
c                  K  P  Q  G  G  *
```

FIG. 14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AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCCTCCATGAATGAGAACGG
M G G T Y S C H
ACTTCGGCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGGACA
TGAAGCCGGGCGACTGAACCCATACATTCGGTGTTCCCCCACCCCCTCCGCCCCCCCTGT
F G P L T W V C K P Q G G G G G G G D K
AAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTTTTCC
TTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGG
T H T C P P C P A P E L L G G P S V F L
TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
AGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGC
F P P K P K D T L M I S R T P E V T C V
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
V V D V S H E D P E V K F N W Y V D G V
TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V
TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
ACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGT
V S V L T V L H Q D W L N G K E Y K C K
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
TCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q
AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q
AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
TCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC
V S L T C L V K G F Y P S D I A V E W E
AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
TCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G
GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
CGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGC
S F F L Y S K L T V D K S R W Q Q G N V
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S
BamHI
CCCTGTCTCCGGGTAAATAATGGATCC
GGGACAGAGGCCCATTTATTACCTAGG
L S P G K *

FIG. 15

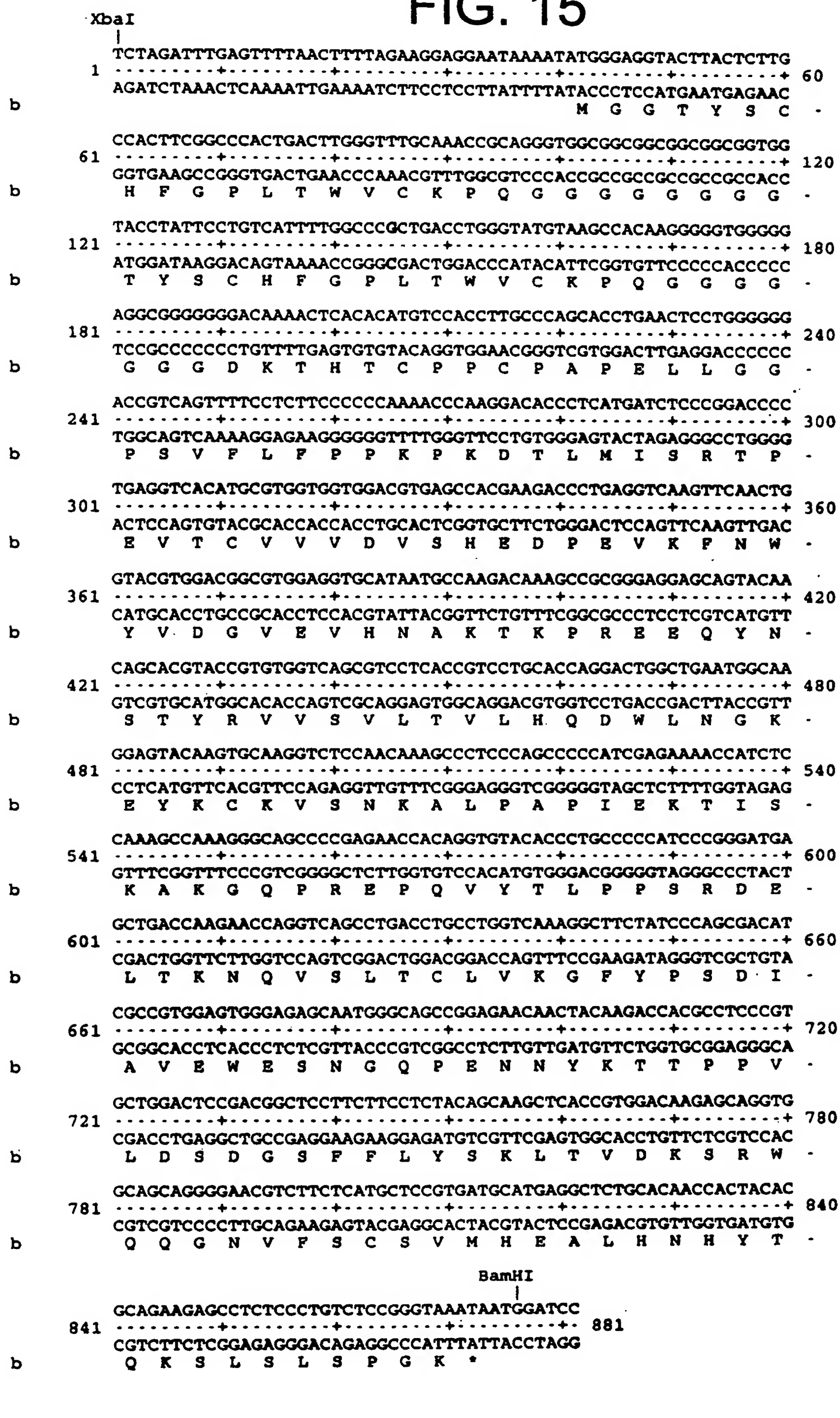


FIG. 16

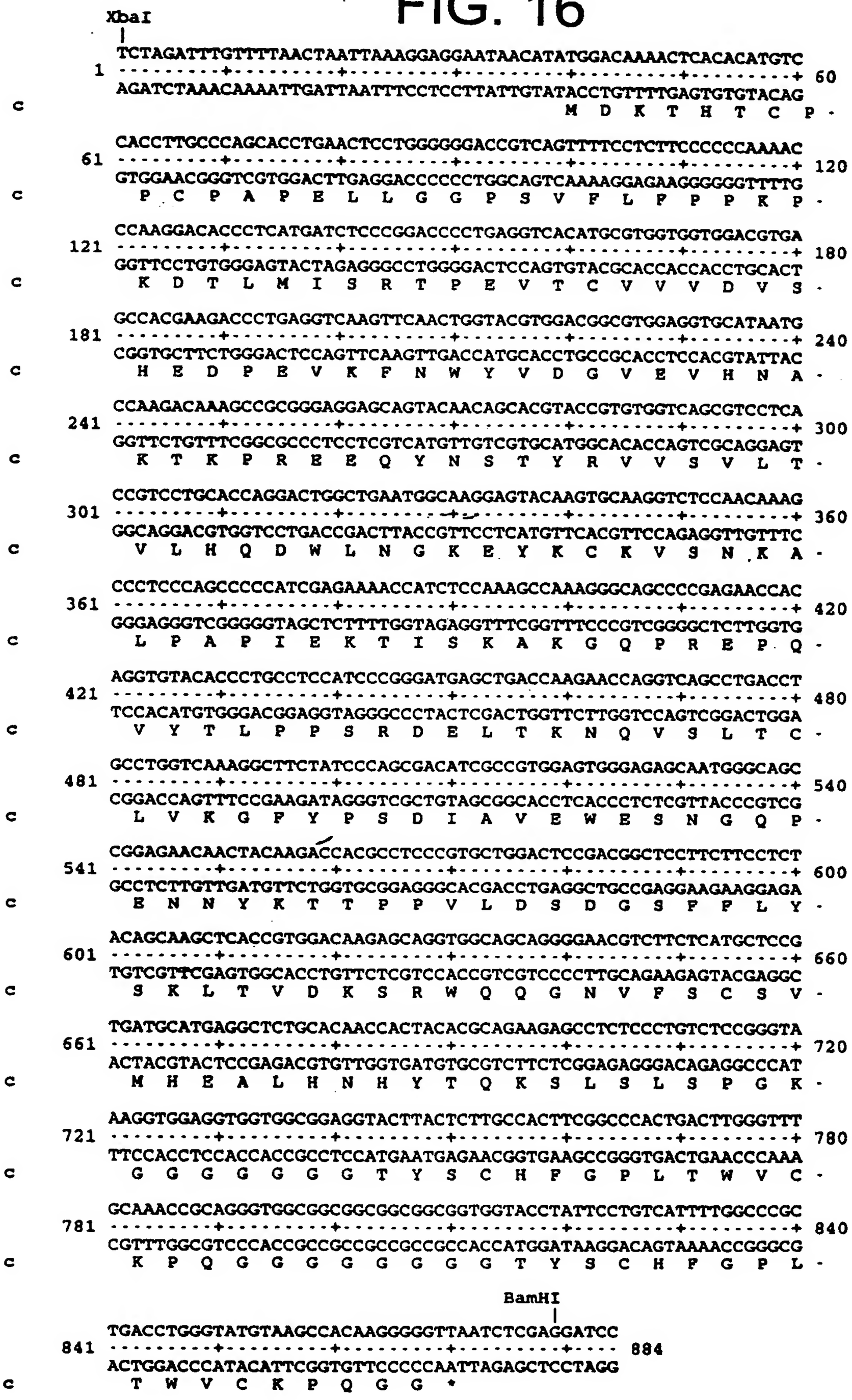


FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA-

-GGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG-

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCTCCCACCGCCCGTCCTGCGGGCG-

-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT-
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-

AatII
-TTCTACAAACTCTTTTGTTTATTTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC-
-AAAATTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-

-GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCCTTCGCATGCCCACGCTAAAC-
-ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-

-ATTCTTTTTTCTCTTTTGGTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTTC-
-TAAGAAAAAGAGAAAACCAATTTAGCAACAAACTAAATAATAAACGATATAAATAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTCATACACGCATGTAAAAATA-
-CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-

-AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAAACTAAGCATTCCGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA-

-TAGCAGTATGAATAGGGAAACTAAACCCAGTGATAAGACCTGATGATTTCGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-

-TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-

-AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACTTTATAGTCTAAATTGGTATC-

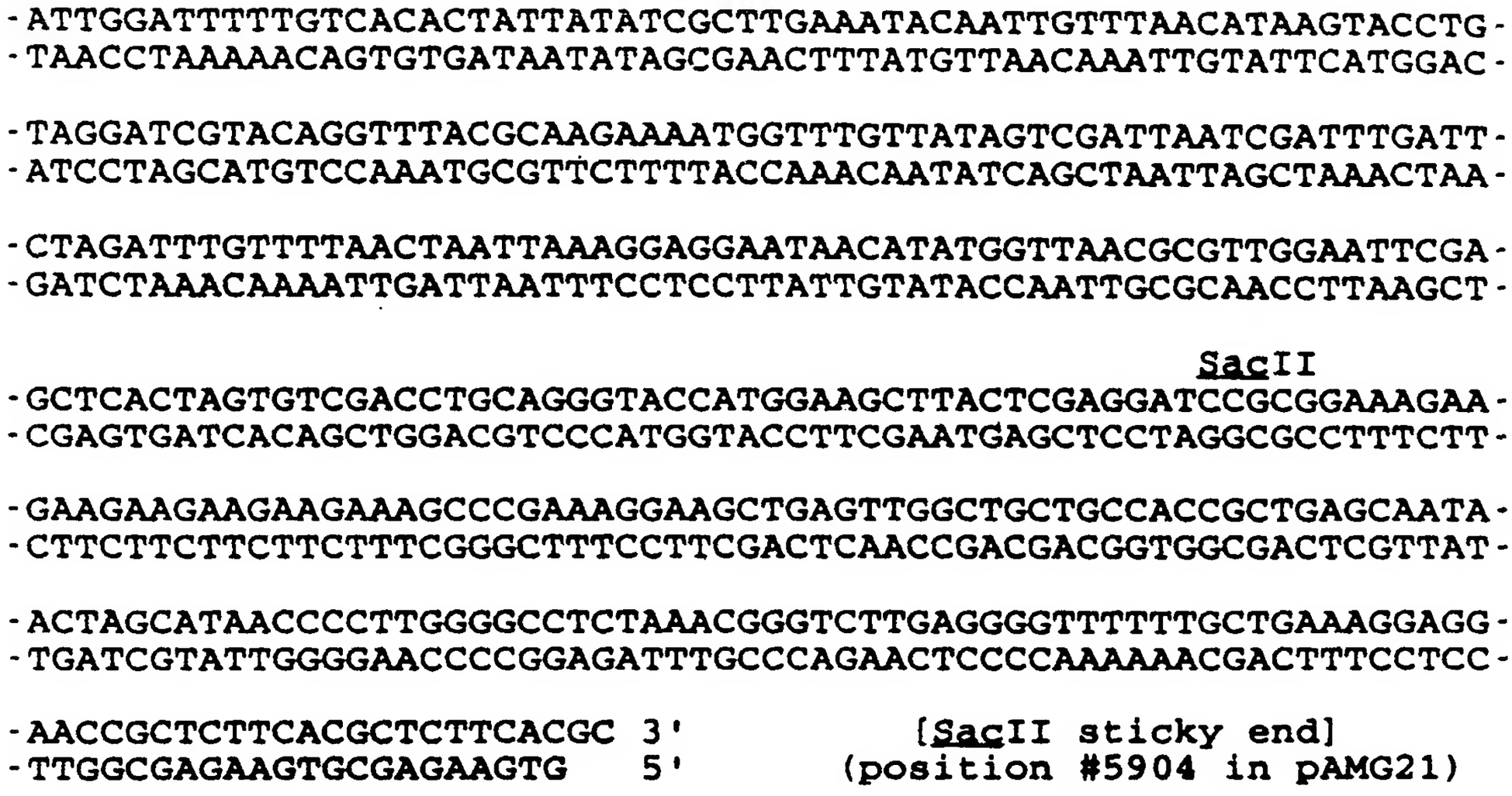
-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAAATCAGTATAGTC-

-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-
-TATTCGTAACTAATTATAGTAATAACGAAGATGTCCGAAATTAAAATAATTAATAAGACA-

-AAGTGTCGTCGGCATTTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-

-GCAAGTTTTGCGTGTTATATATCATTAAAACGGTAATAGATTGACATTTGATTCTAATAA-
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

FIG. 17B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-TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC-
-TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGATTAATCGATTTGATT-
-ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA-
-CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA-
-GATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT-
SacII
-GCTCACTAGTGTCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA-
-CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT-
-GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA-
-CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT-
-ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGG-
-TGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAAACGACTTTCCTCC-
-AACCGCTCTTCACGCTCTTCACGC 3'
-TTGGCGAGAAGTGCGAGAAGTG 5'
[SacII sticky end]
(position #5904 in pAMG21)

FIG.18A - 1

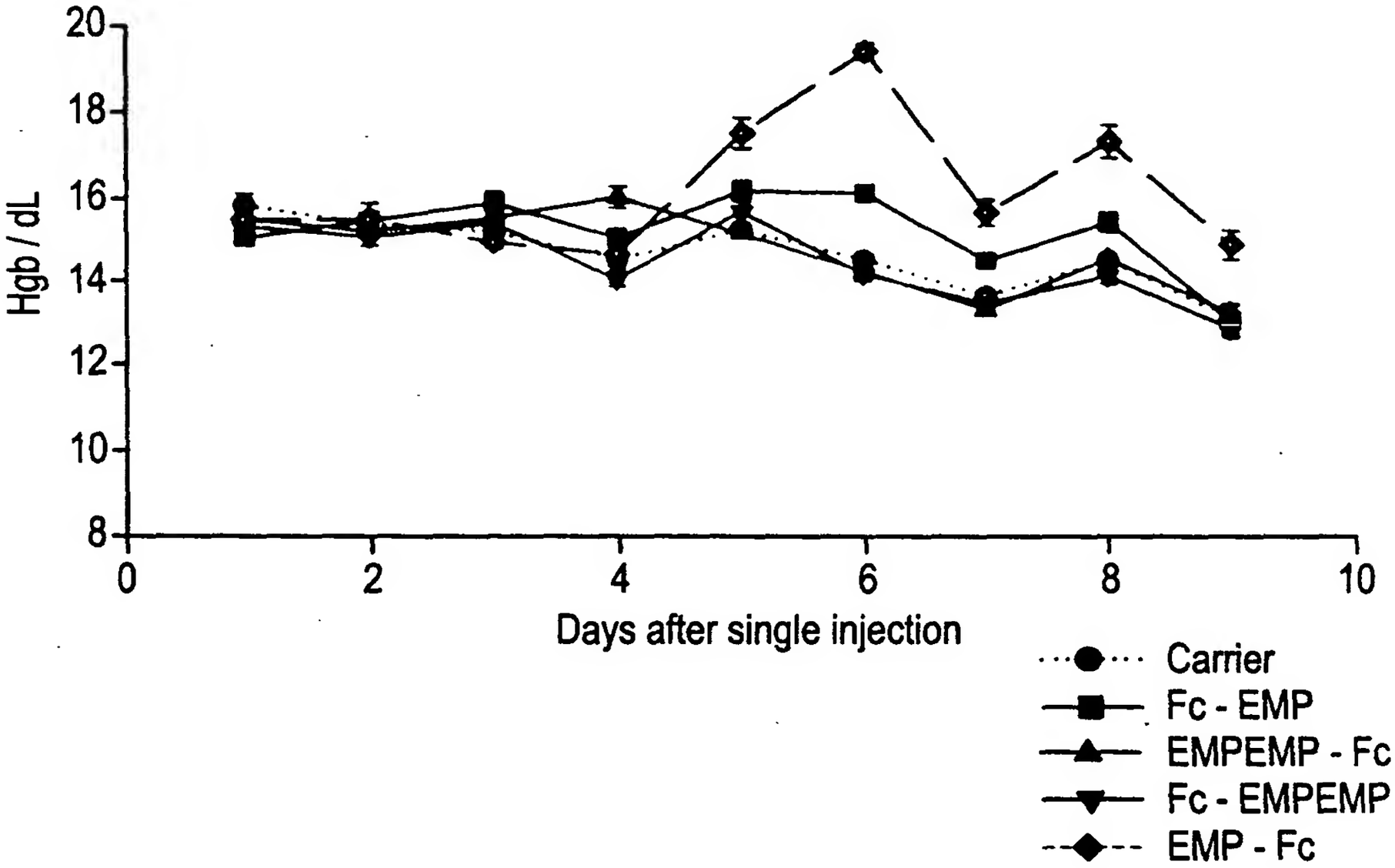


FIG.18A - 2

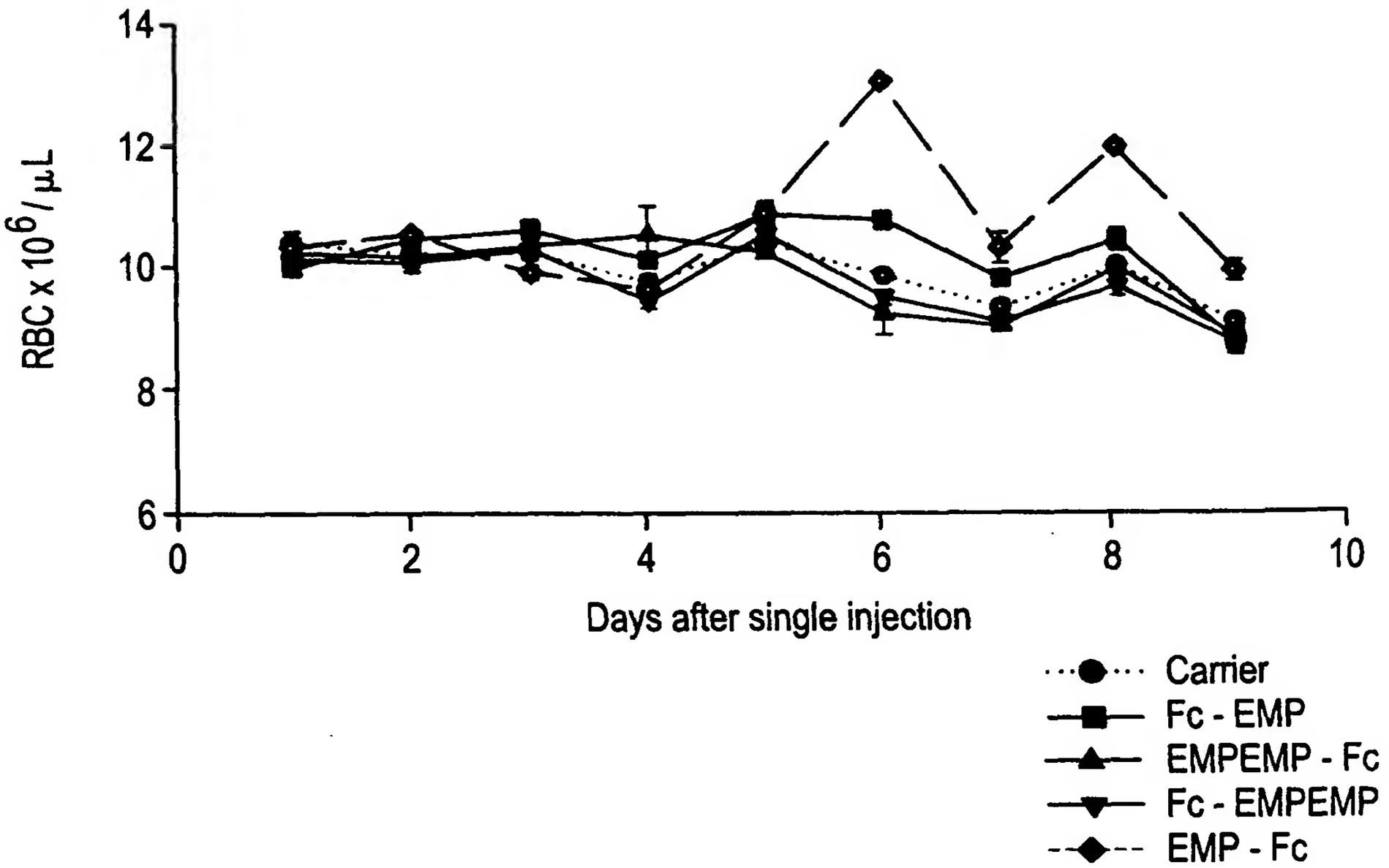


FIG.18A - 3

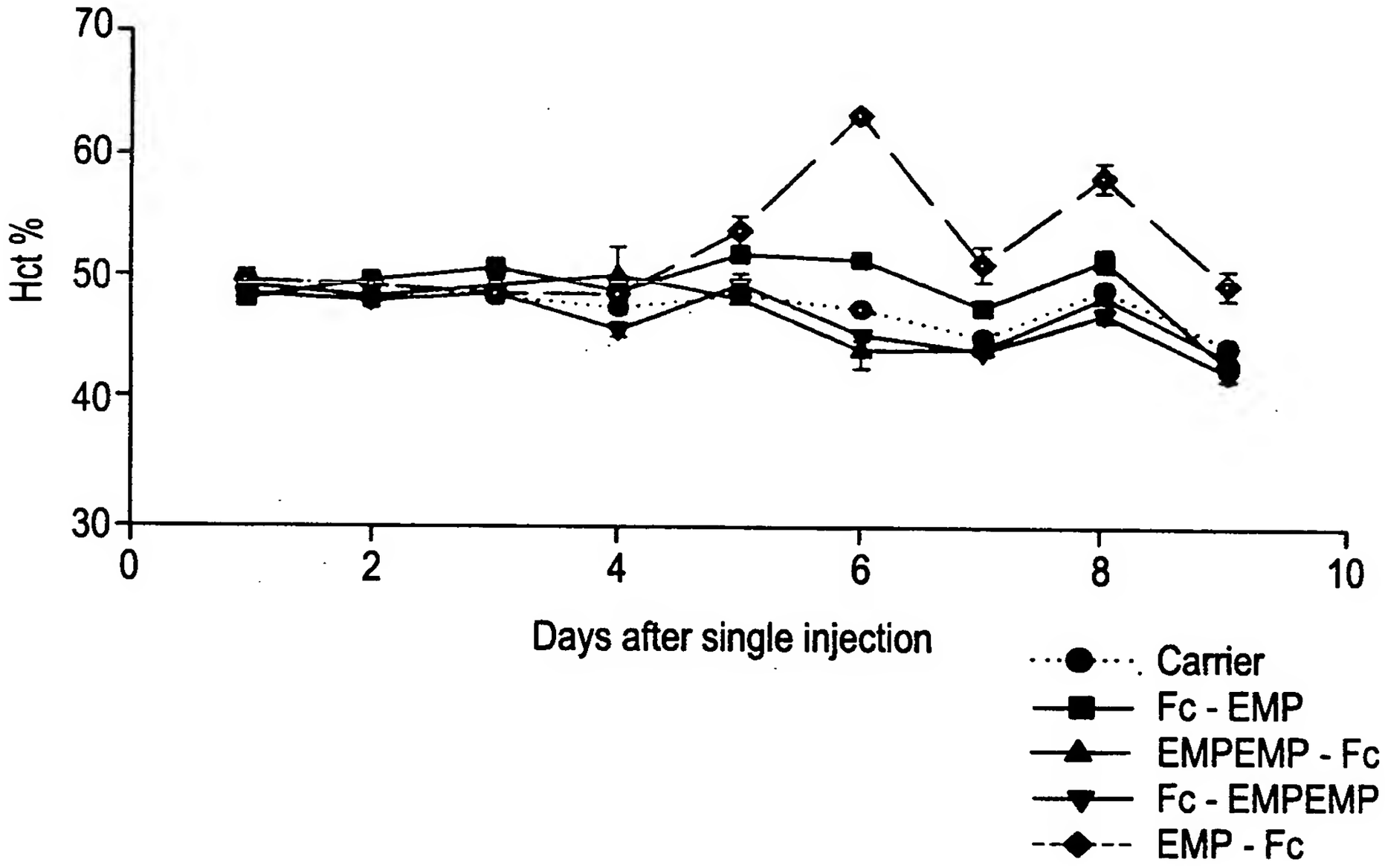


FIG.18B - 1

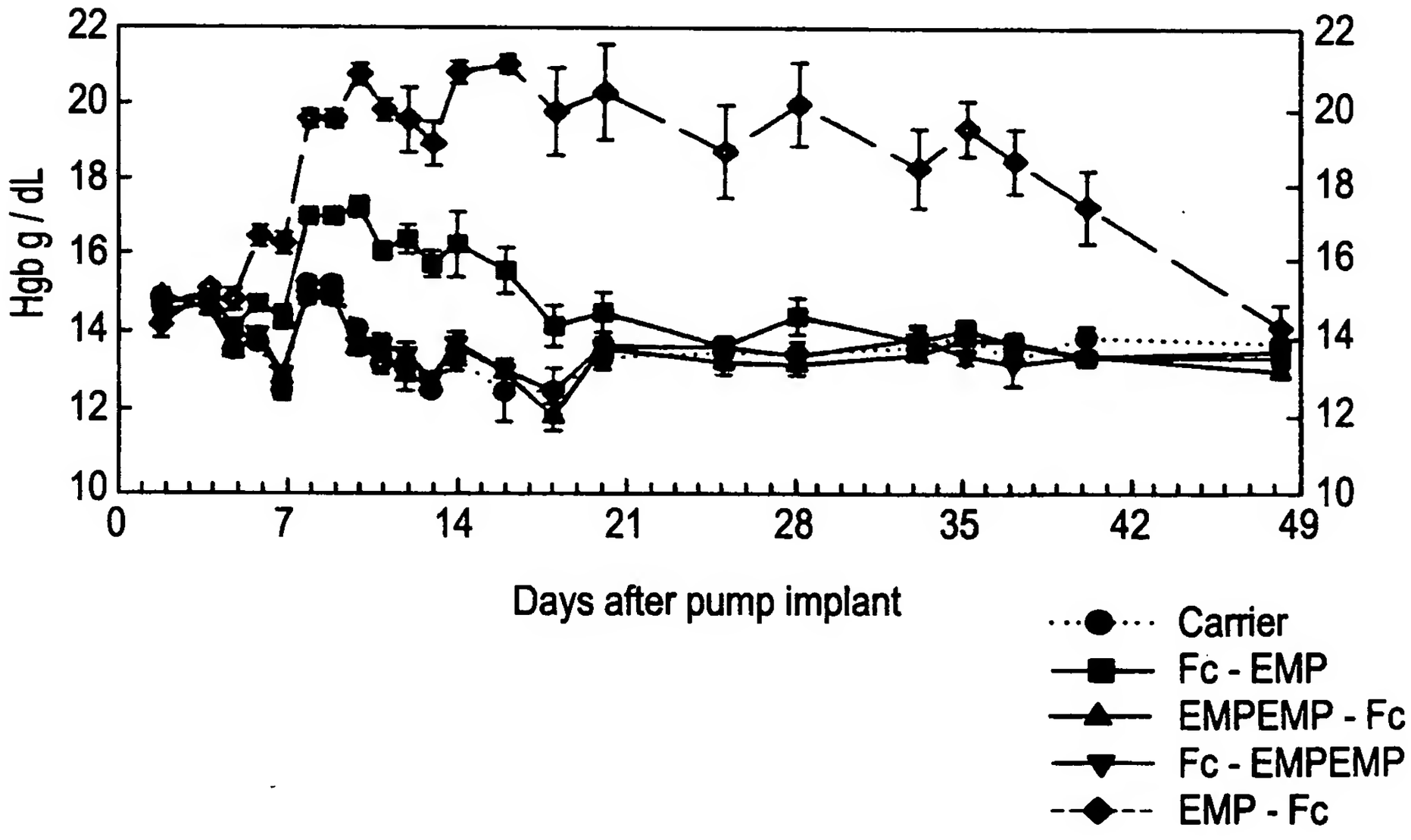


FIG.18B - 2

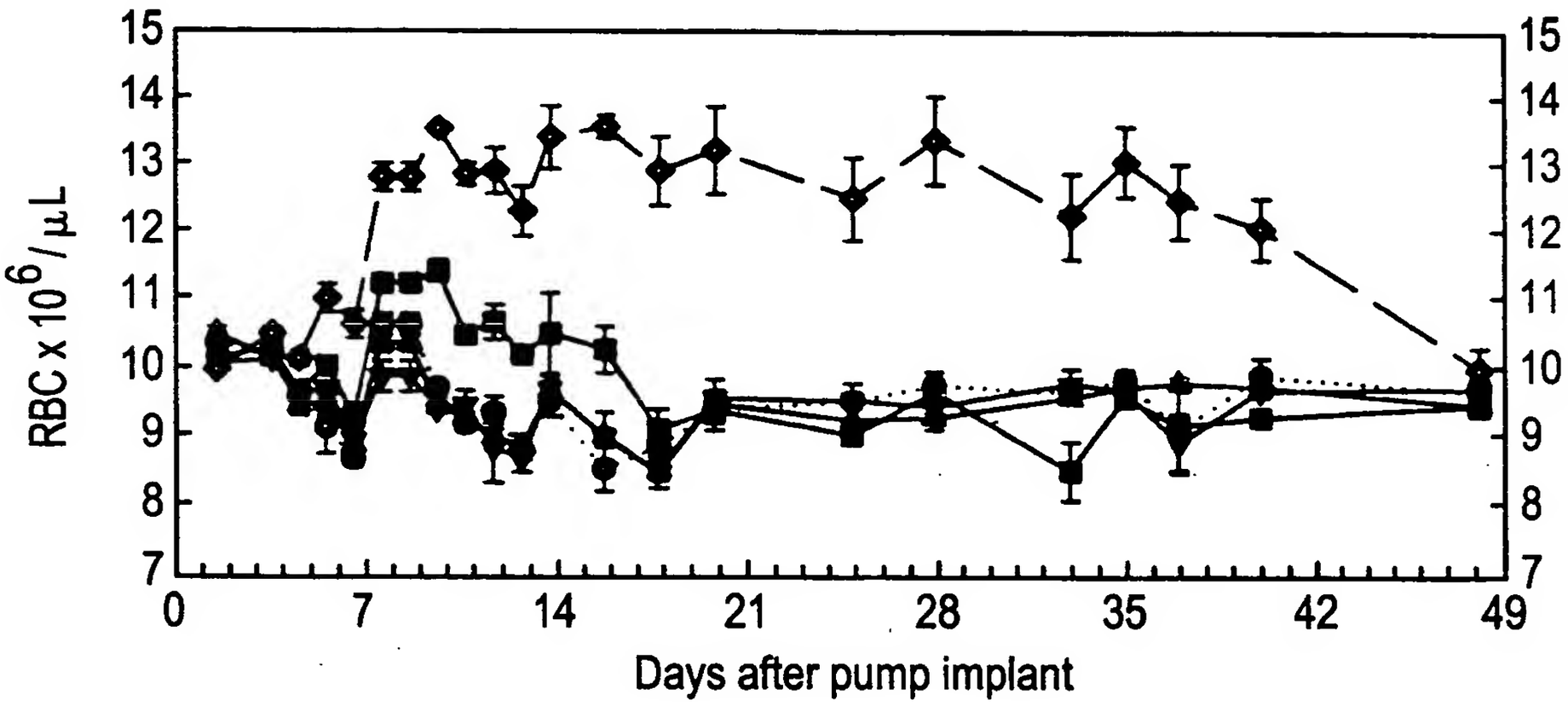


FIG.18B - 3

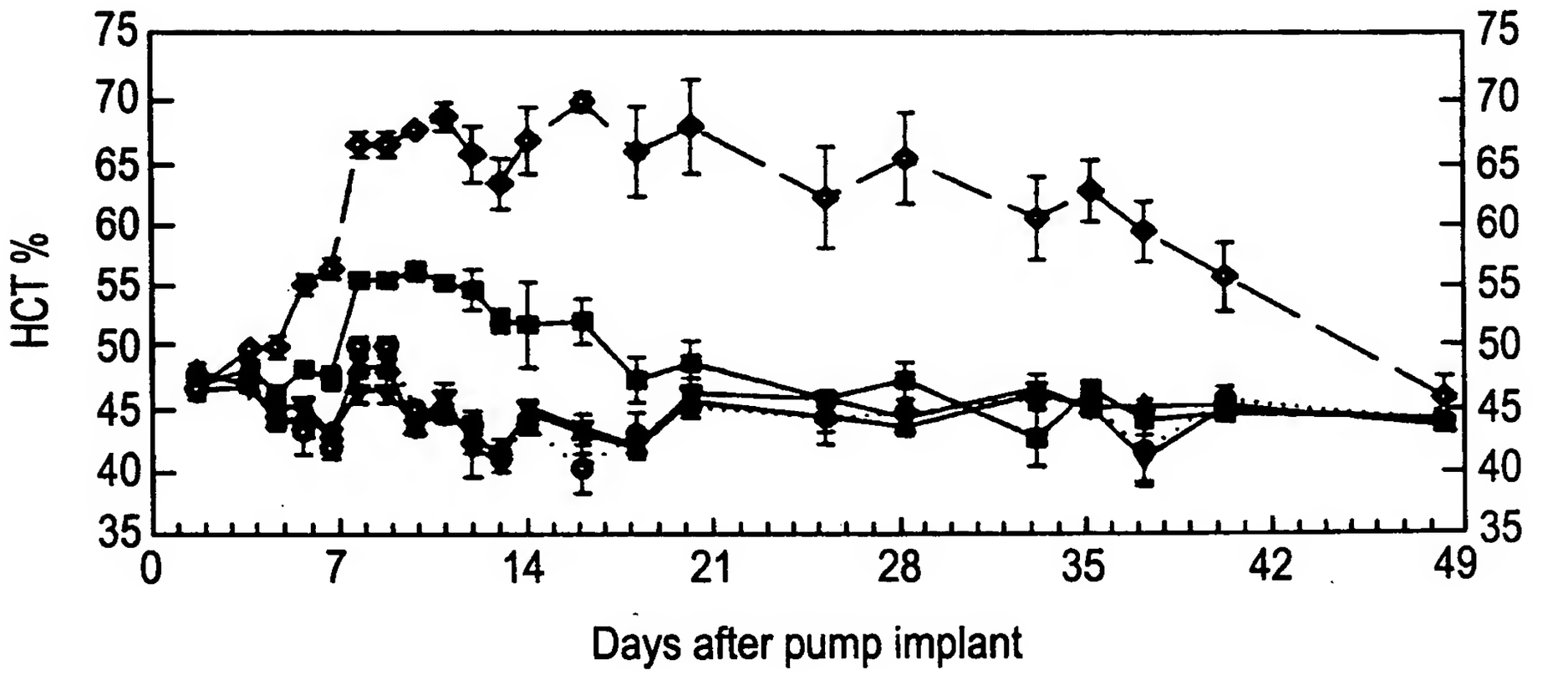
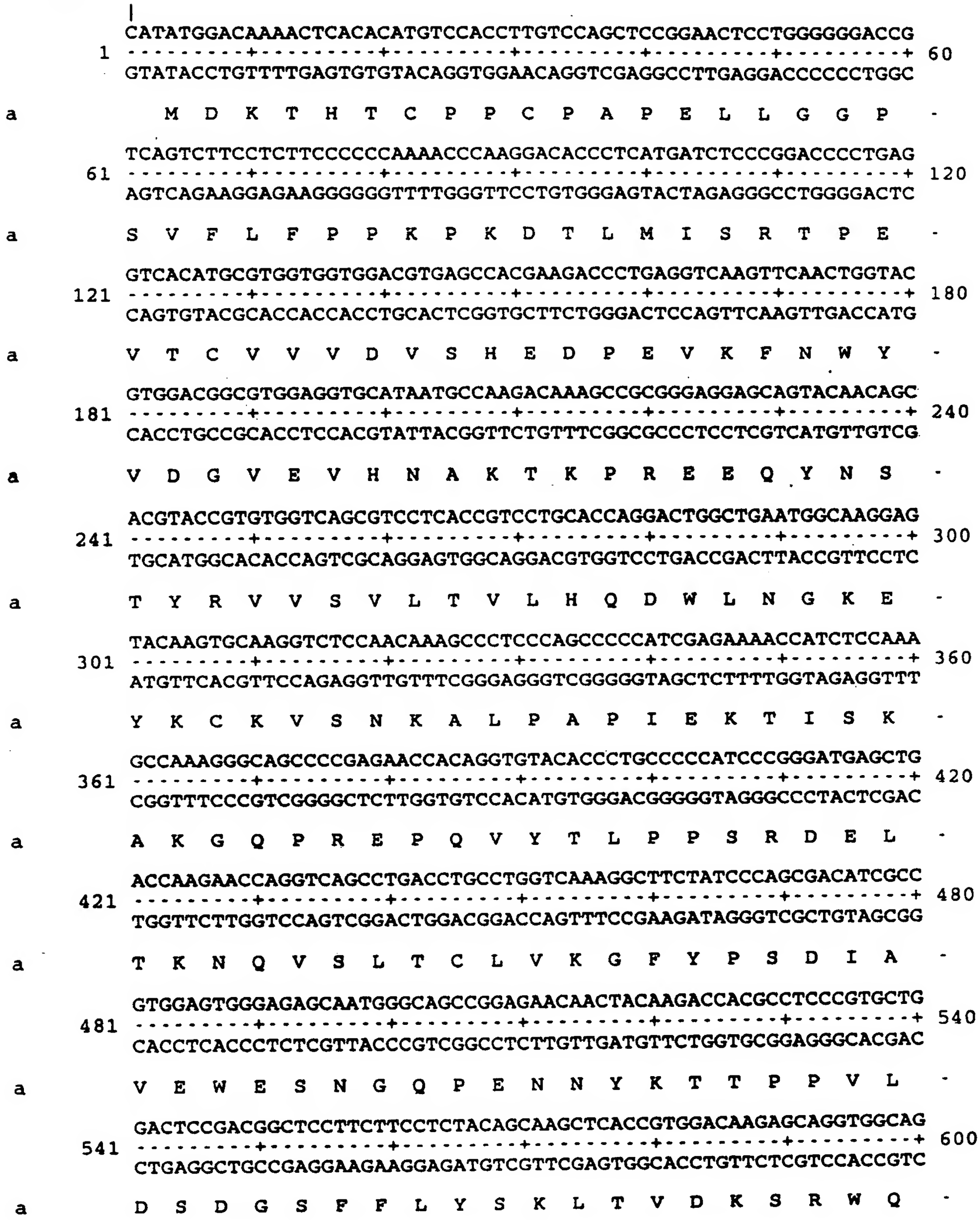


FIG. 19A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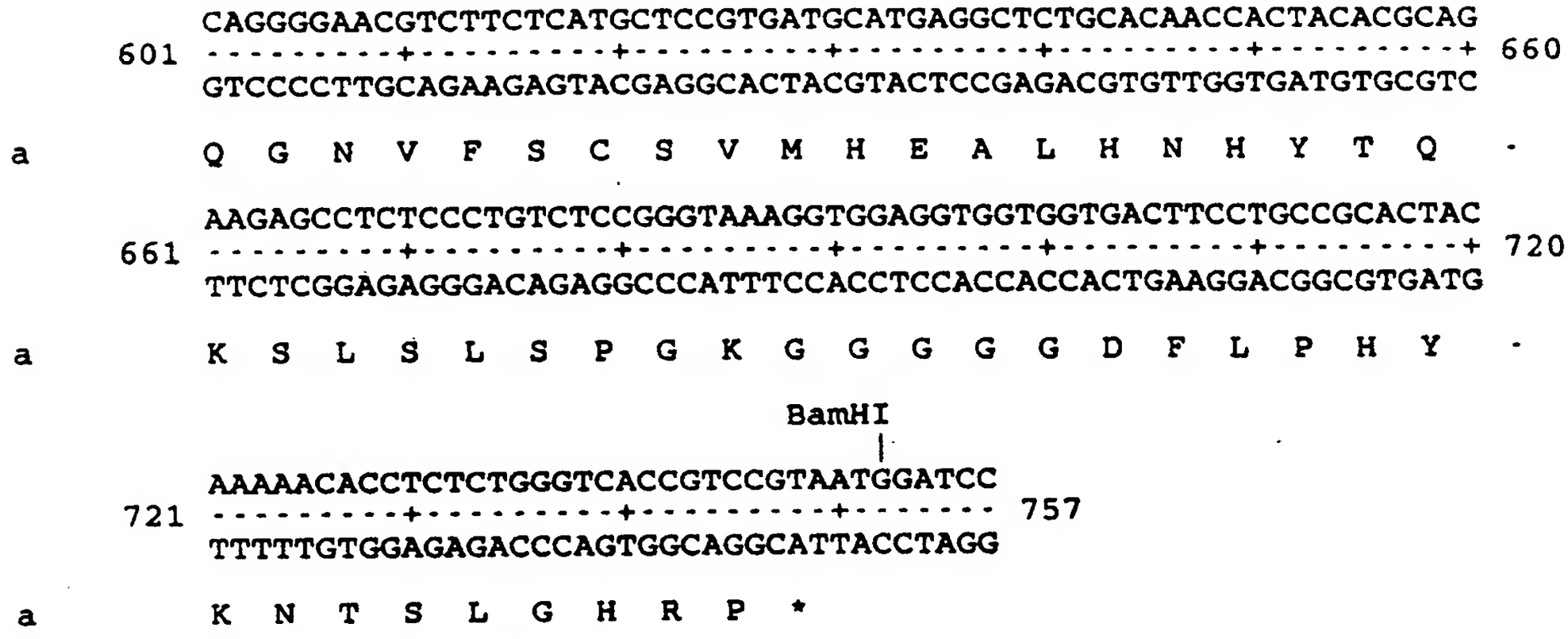
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 19B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601 + 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q ·
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
661 + 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG
a K S L S L S P G K G G G G G D F L P H Y ·
BamHI
AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
721 + 757
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG
a K N T S L G H R P *

TITLE: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
INVENTORS: FEIGE, et al.
APPLN. NO: A-527H

FIG. 20A

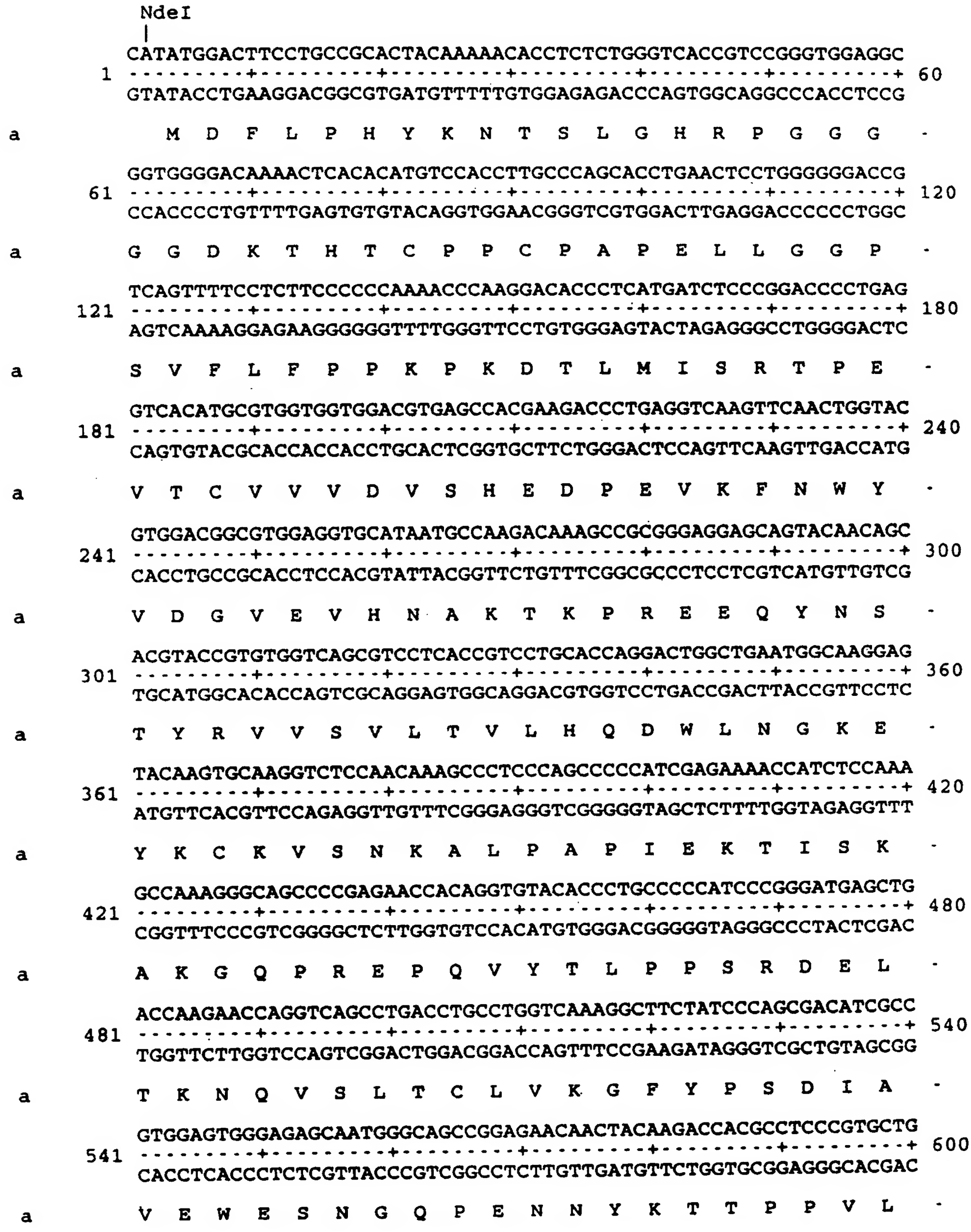


FIG. 20B


GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
601 ---------+---------+---------+---------+---------+---------+---------+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661 ---------+---------+---------+---------+---------+---------+---------+ 720
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
BamHI
AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
721 ---------+---------+---------+---------+---------+-- 761
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC
a K S L S L S P G K *

FIG. 21A

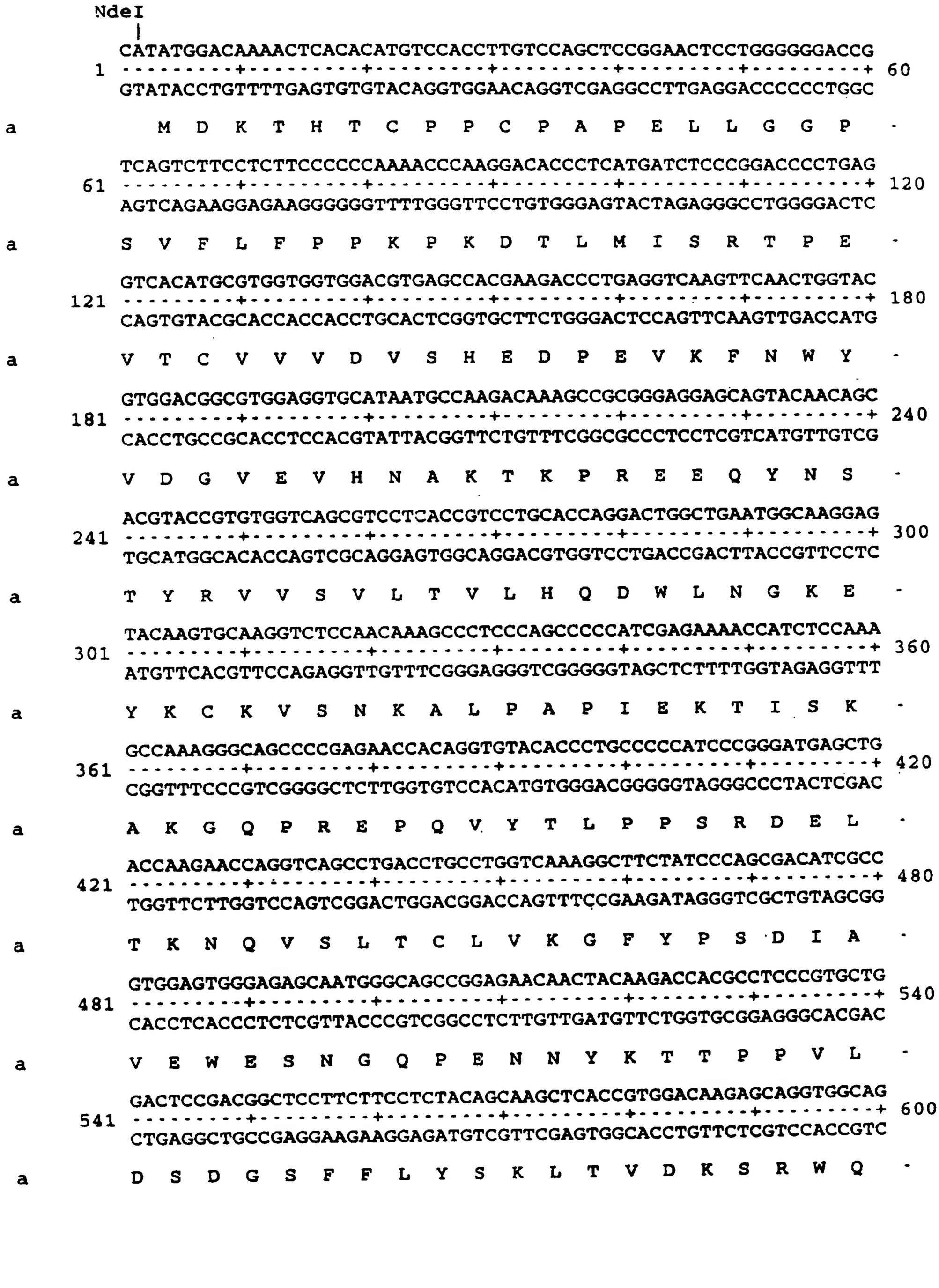

NdeI
CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG
1 ---------+---------+---------+---------+---------+---------+---------+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 ---------+---------+---------+---------+---------+---------+---------+ 120
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 ---------+---------+---------+---------+---------+---------+---------+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 ---------+---------+---------+---------+---------+---------+---------+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 ---------+---------+---------+---------+---------+---------+---------+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 ---------+---------+---------+---------+---------+---------+---------+ 360
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 ---------+---------+---------+---------+---------+---------+---------+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
421 ---------+---------+---------+---------+---------+---------+---------+ 480
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
481 ---------+---------+---------+---------+---------+---------+---------+ 540
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 ---------+---------+---------+---------+---------+---------+---------+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 21B

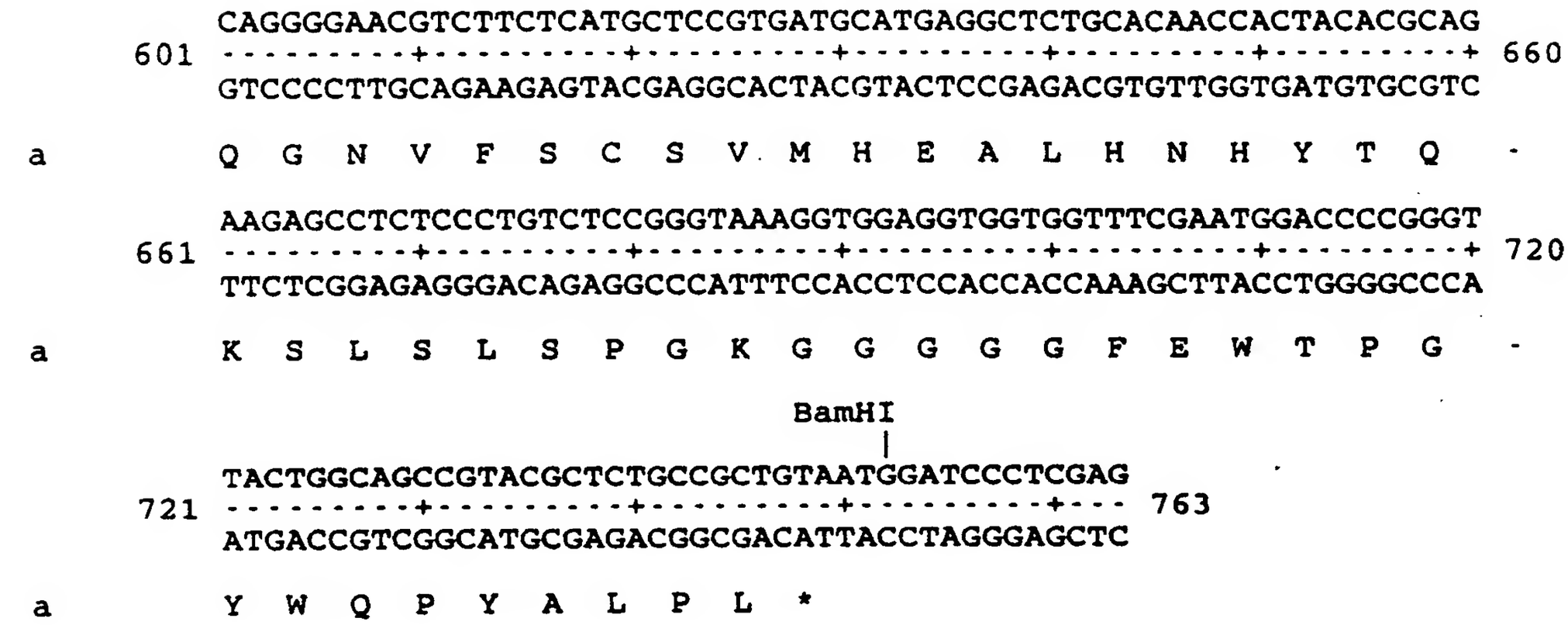

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 ---------+---------+---------+---------+---------+---------+---------+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
661 ---------+---------+---------+---------+---------+---------+---------+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA
a K S L S L S P G K G G G G G F E W T P G -
BamHI
TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
721 ---------+---------+---------+---------+---------+--- 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC
a Y W Q P Y A L P L *

FIG. 22A

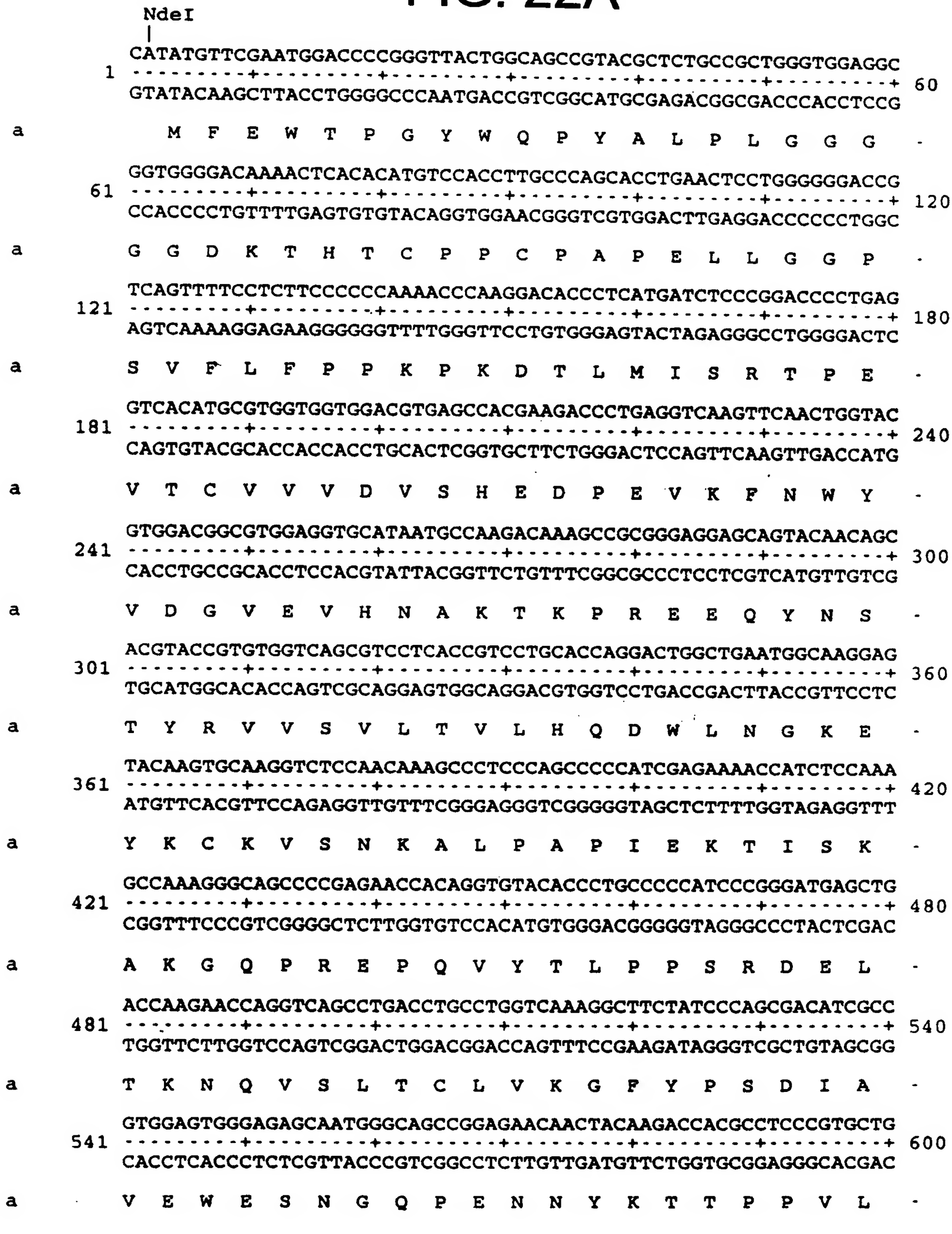

NdeI
CATATGTTCGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG
a M F E W T P G Y W Q P Y A L P L G G G .
GGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P .
TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E .
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y .
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S .
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E .
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K .
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L .
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A .
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L .

FIG. 22B

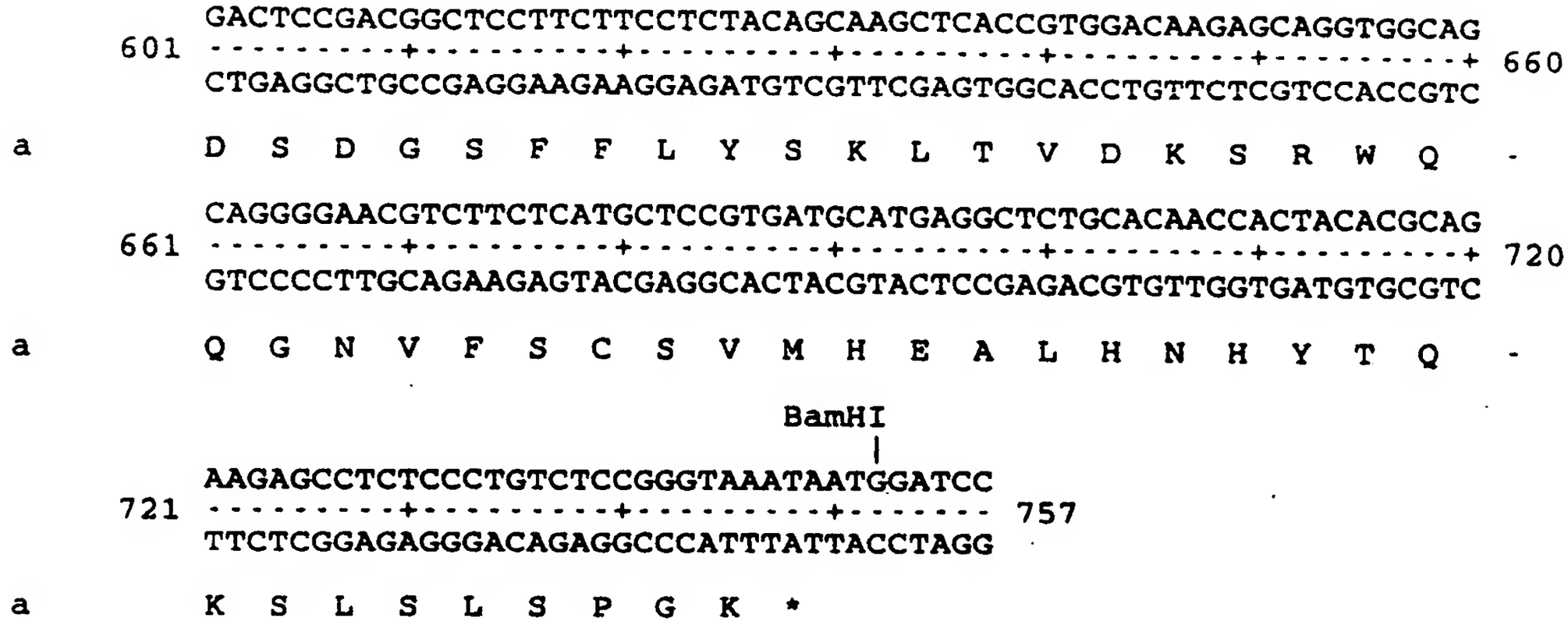

GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
601
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
660
a D S D G S F F L Y S K L T V D K S R W Q -
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
720
a Q G N V F S C S V M H E A L H N H Y T Q -
BamHI
AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
757
a K S L S L S P G K *

FIG. 23A

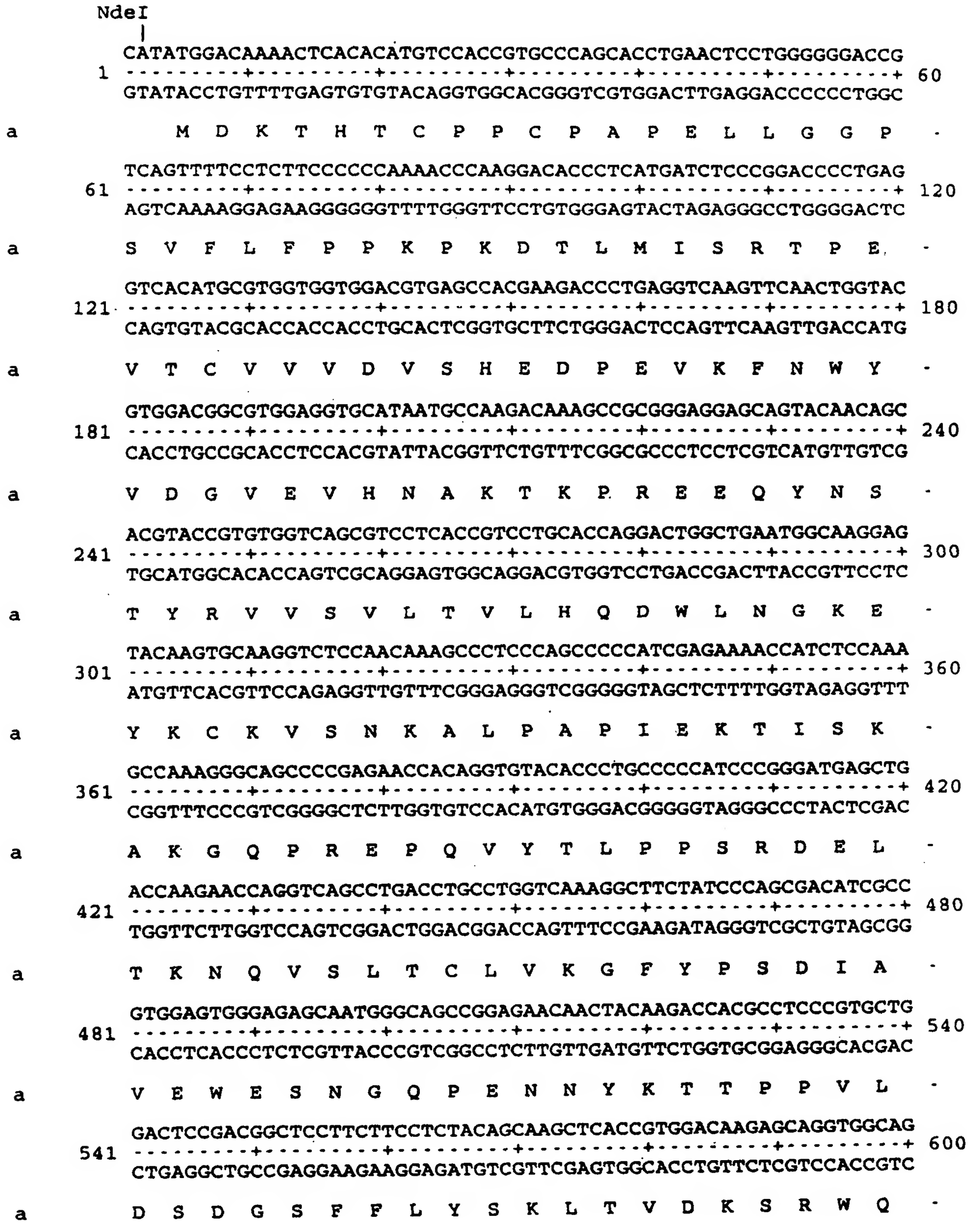
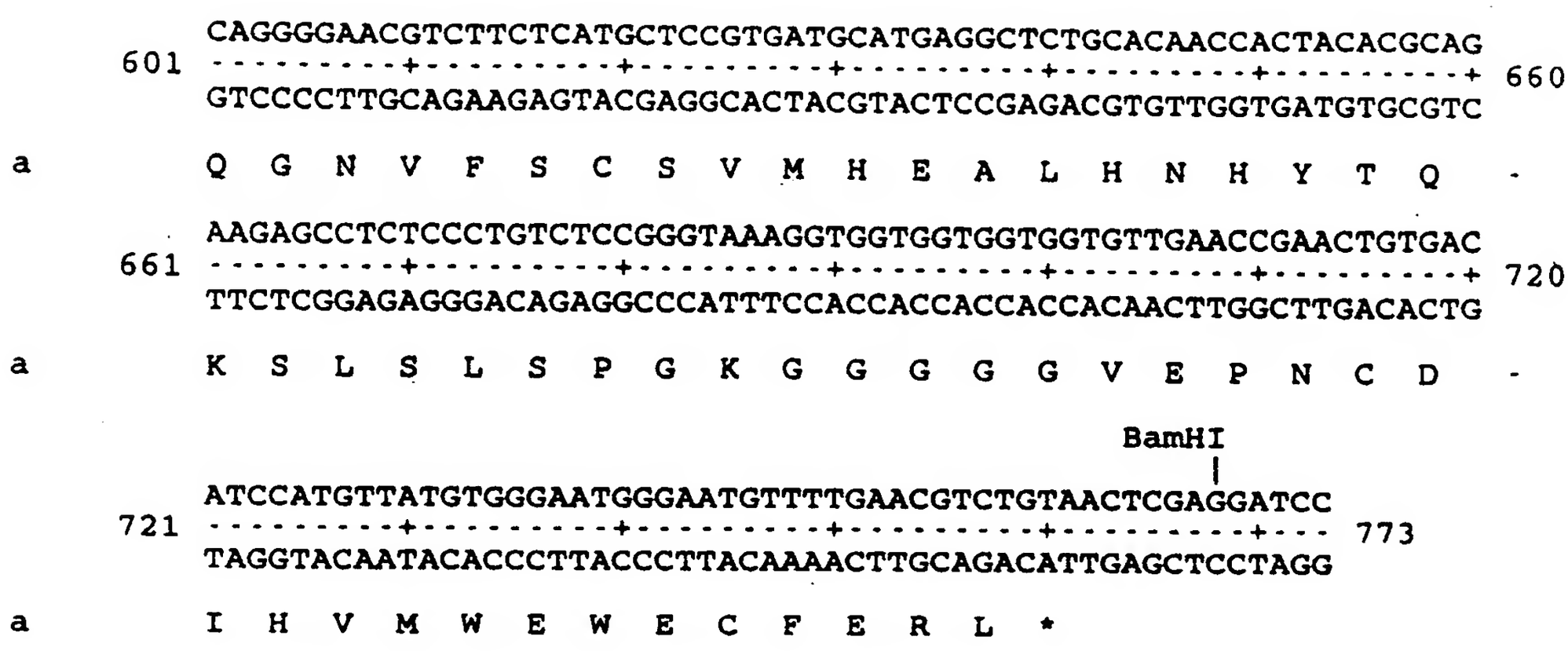

NdeI
CATATGGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B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601
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
660
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGTTGAACCGAACTGTGAC
661
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACTTGGCTTGACACTG
720
a K S L S L S P G K G G G G G V E P N C D -
BamHI
ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACTCGAGGATCC
721
TAGGTACAATACACCCTTACCCTTACAAAACTTGCAGACATTGAGCTCCTAGG
773
a I H V M W E W E C F E R L *

FIG. 24A

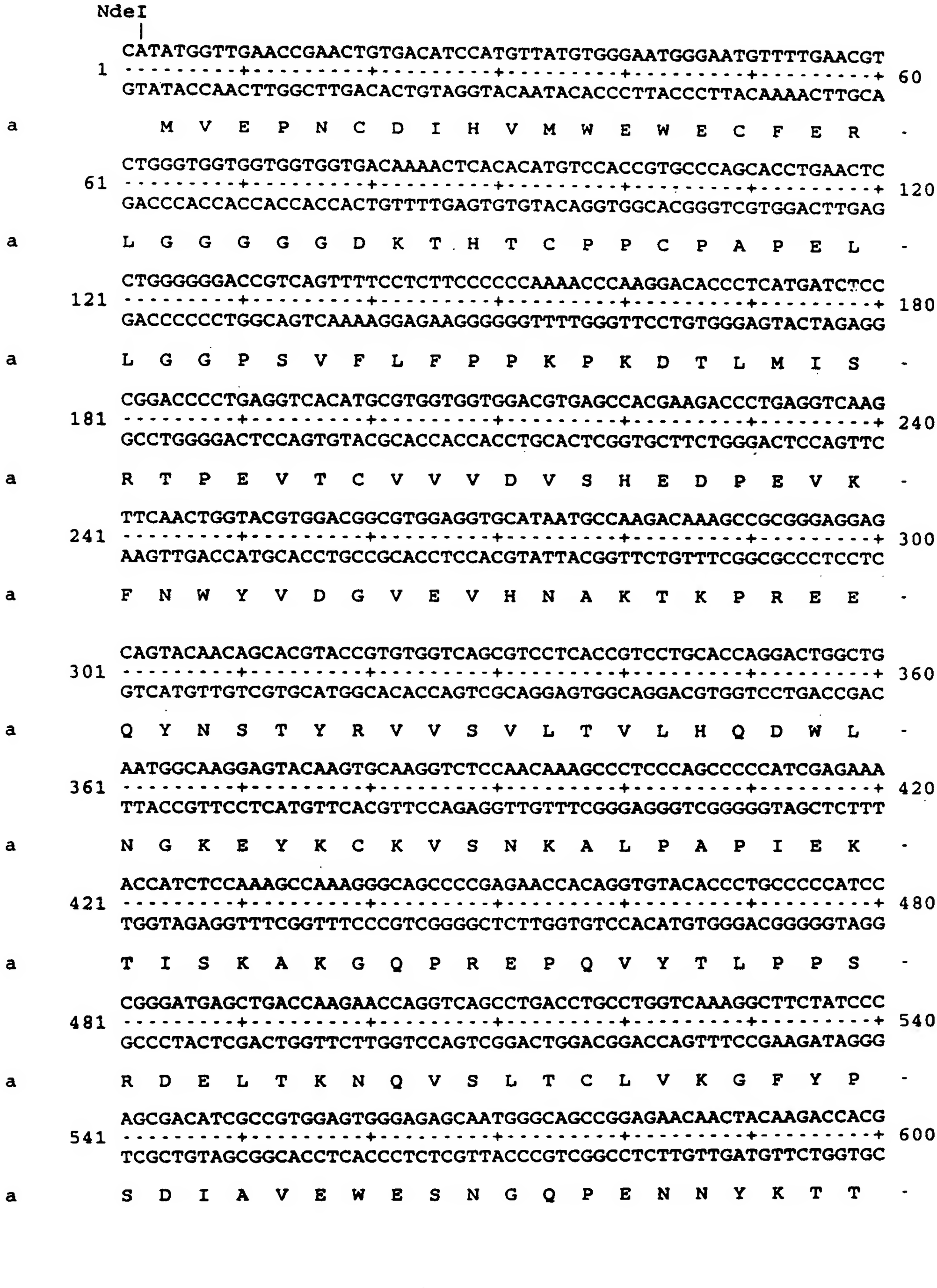

NdeI
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACTTGCA
a M V E P N C D I H V M W E W E C F E R -
CTGGGTGGTGGTGGTGGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTC
GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG
a L G G G G G D K T H T C P P C P A P E L -
CTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC
GACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG
a L G G P S V F L F P P K P K D T L M I S -
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC
a R T P E V T C V V V D V S H E D P E V K -
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC
a F N W Y V D G V E V H N A K T K P R E E -
CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC
a Q Y N S T Y R V V S V L T V L H Q D W L -
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT
a N G K E Y K C K V S N K A L P A P I E K -
ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG
a T I S K A K G Q P R E P Q V Y T L P P S -
CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG
a R D E L T K N Q V S L T C L V K G F Y P -
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG
TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC
a S D I A V E W E S N G Q P E N N Y K T T -

FIG. 24B

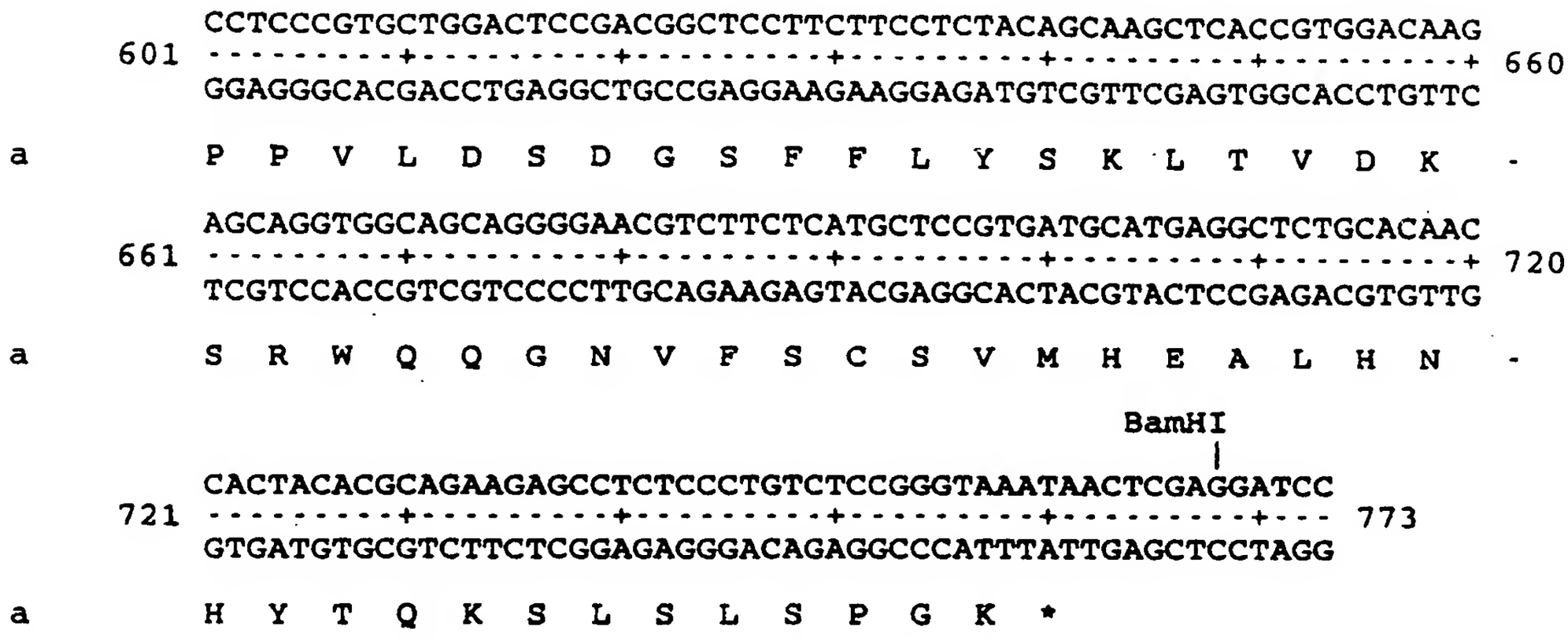

CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG
601
660
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC
a P P V L D S D G S F F L Y S K L T V D K -
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
661
720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a S R W Q Q G N V F S C S V M H E A L H N -
BamHI
CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
721
773
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a H Y T Q K S L S L S P G K *

FIG. 25A

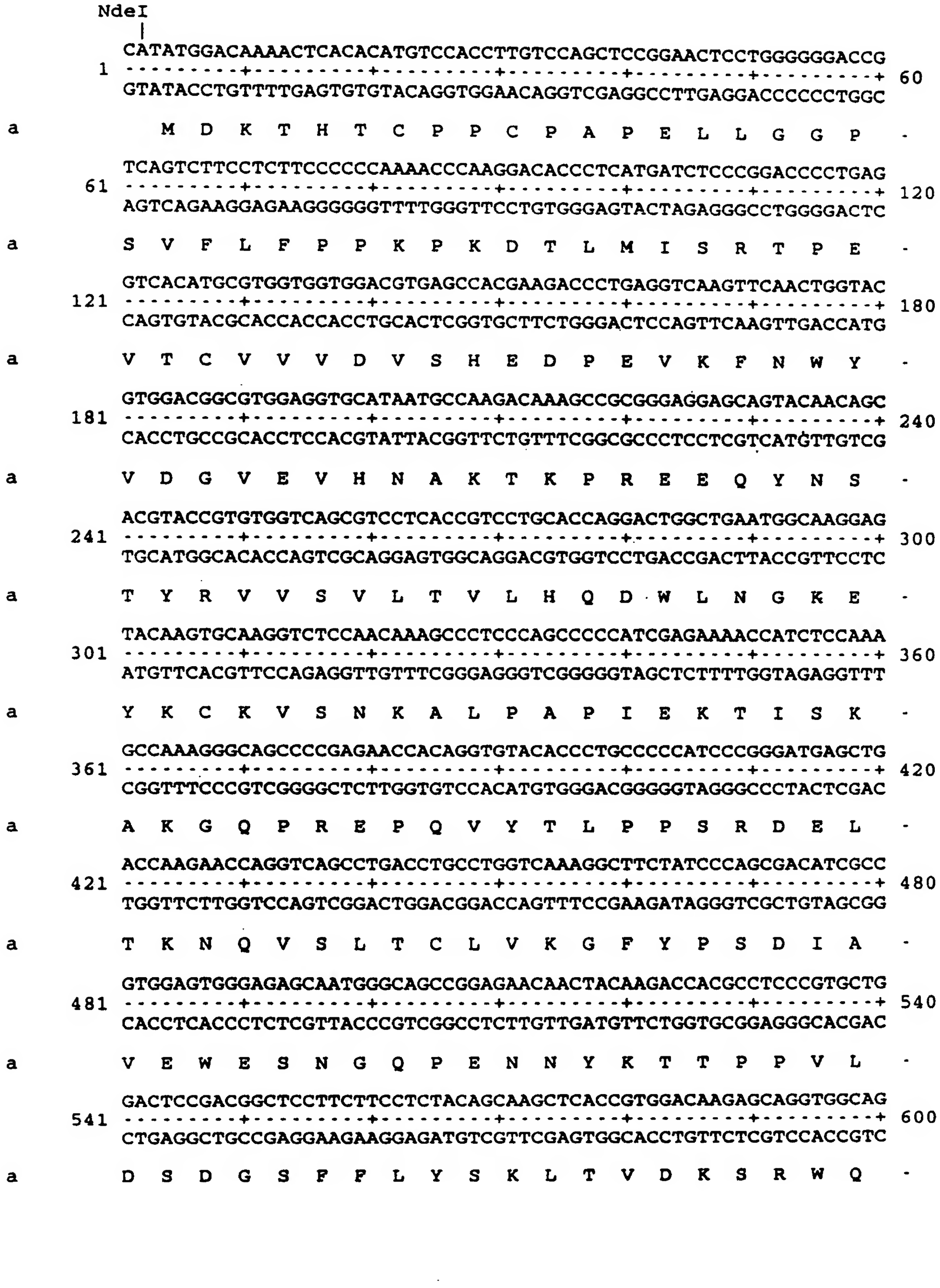
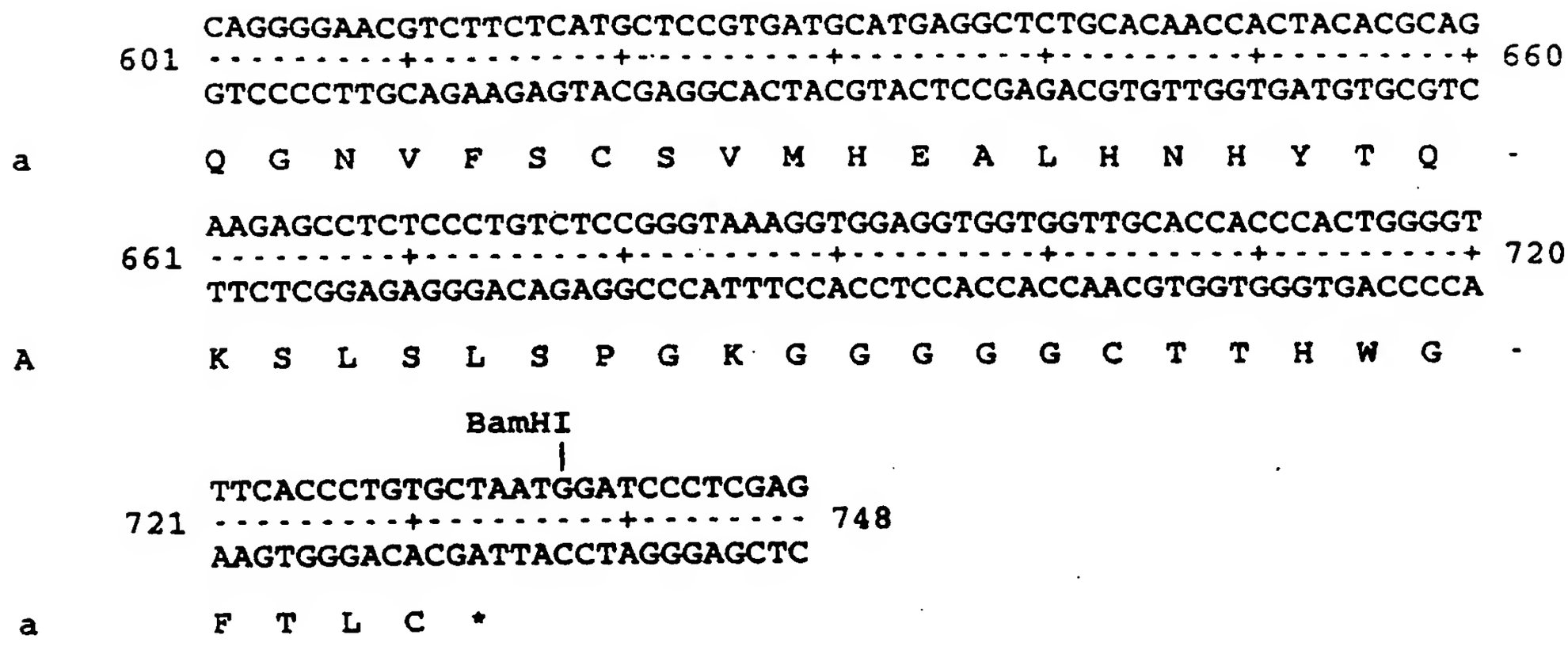

NdeI
CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
121
180
181
240
241
300
301
360
361
420
421
480
481
540
541
600

FIG. 25B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601 ---------+---------+---------+---------+---------+---------+---------+ 660
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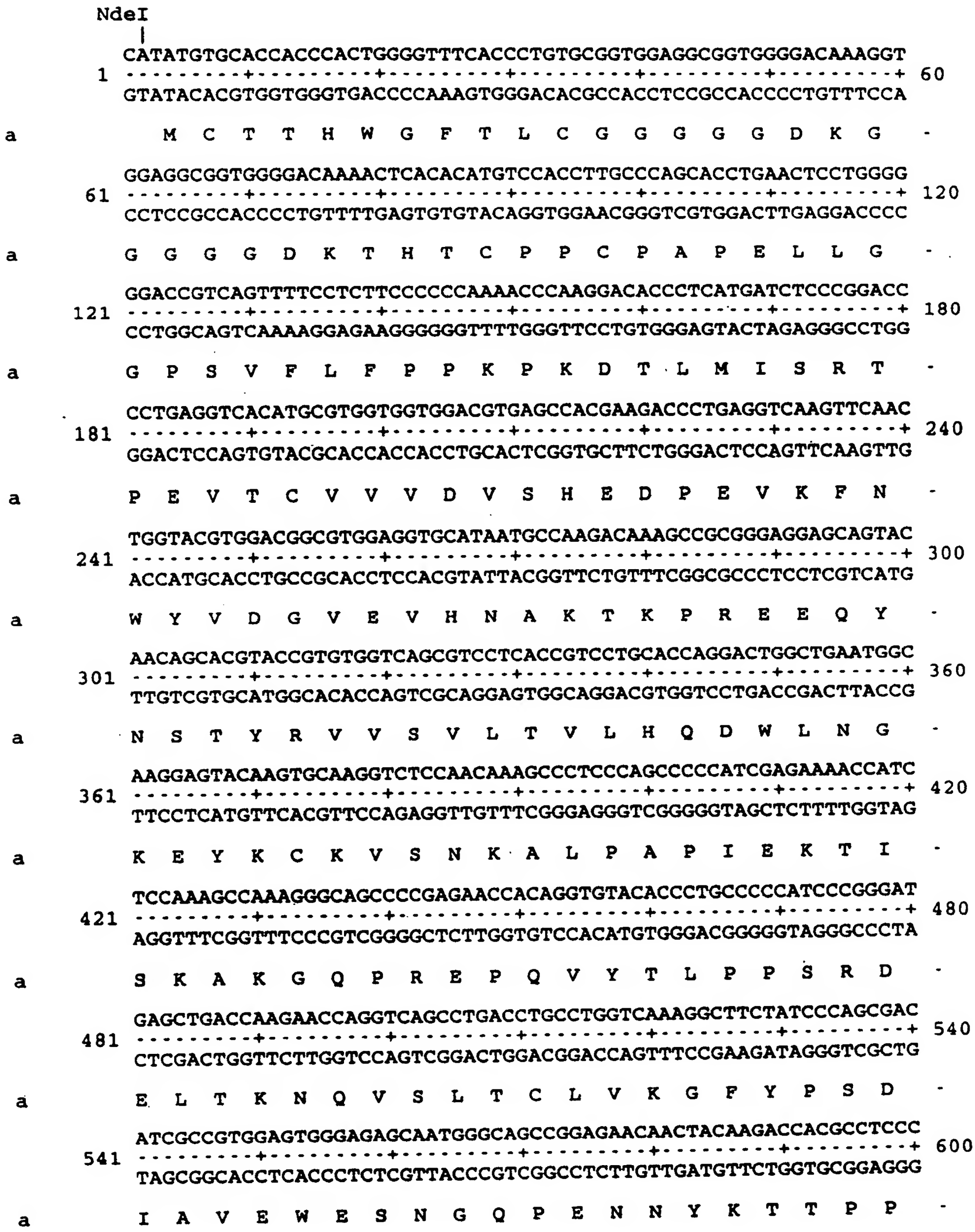
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
661 ---------+---------+---------+---------+---------+---------+---------+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA
A K S L S L S P G K G G G G G C T T H W G -
BamHI
TTCACCCTGTGCTAATGGATCCCTCGAG
721 ---------+---------+--------- 748
AAGTGGGACACGATTACCTAGGGAGCTC
a F T L C *

FIG. 26A


NdeI
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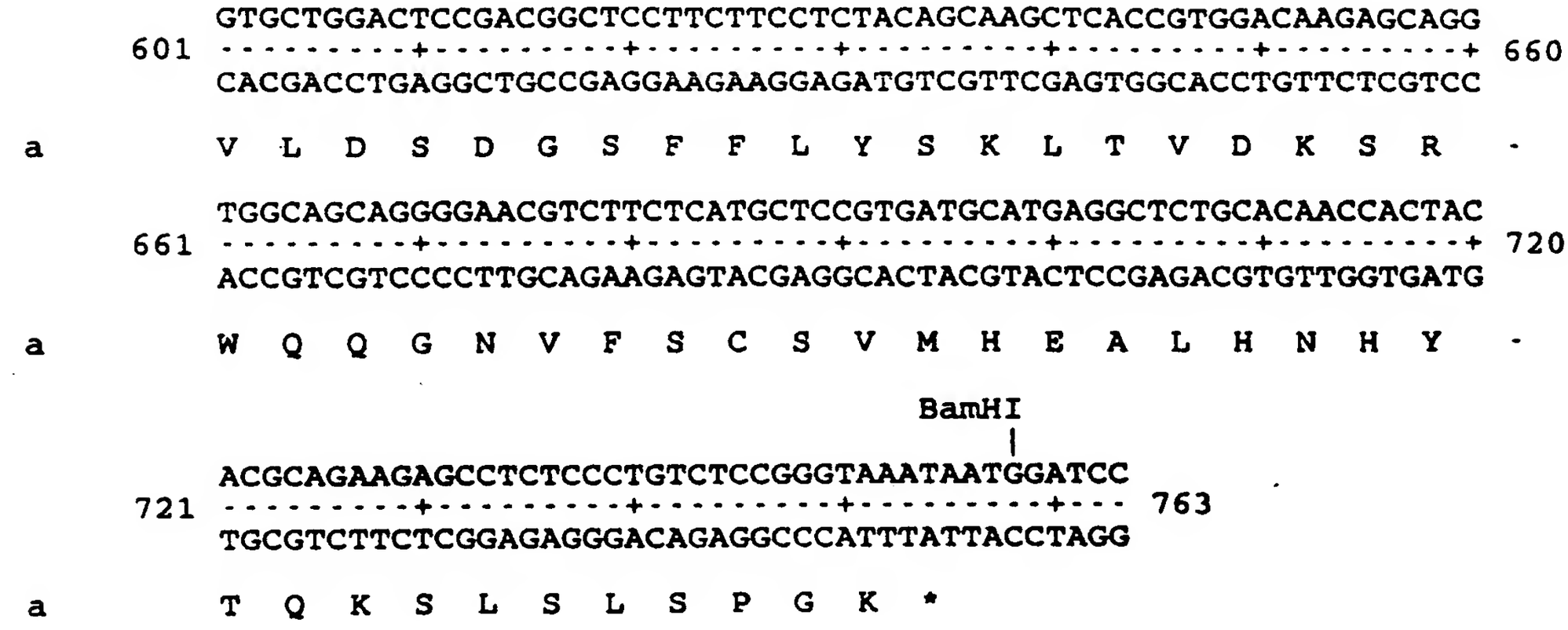
1 ---------+---------+---------+---------+---------+---------+---------+ 60
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA
a M C T T H W G F T L C G G G G G D K G -
GGAGGCGGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG
61 ---------+---------+---------+---------+---------+---------+---------+ 120
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCC
a G G G G D K T H T C P P C P A P E L L G -
GGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
121 ---------+---------+---------+---------+---------+---------+---------+ 180
CCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG
a G P S V F L F P P K P K D T L M I S R T -
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
181 ---------+---------+---------+---------+---------+---------+---------+ 240
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG
a P E V T C V V V D V S H E D P E V K F N -
TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
241 ---------+---------+---------+---------+---------+---------+---------+ 300
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG
a W Y V D G V E V H N A K T K P R E E Q Y -
AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
301 ---------+---------+---------+---------+---------+---------+---------+ 360
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG
a N S T Y R V V S V L T V L H Q D W L N G -
AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
361 ---------+---------+---------+---------+---------+---------+---------+ 420
TTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG
a K E Y K C K V S N K A L P A P I E K T I -
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
421 ---------+---------+---------+---------+---------+---------+---------+ 480
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA
a S K A K G Q P R E P Q V Y T L P P S R D -
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
481 ---------+---------+---------+---------+---------+---------+---------+ 540
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG
a E L T K N Q V S L T C L V K G F Y P S D -
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCC
541 ---------+---------+---------+---------+---------+---------+---------+ 600
TAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGG
a I A V E W E S N G Q P E N N Y K T T P P -

FIG. 26B


GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
601 + 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCC
a V L D S D G S F F L Y S K L T V D K S R -
TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661 + 720
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a W Q Q G N V F S C S V M H E A L H N H Y -
BamHI
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 + 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a T Q K S L S L S P G K *